

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 05:49:50 ; Search time 4711 Seconds  
(without alignments)  
9941.386 Million cell updates/sec

Title: US-09-615-039-1\_COPY\_13000\_14000

Perfect score: 1001

Sequence: 1 cgtccgacctggaggcagc.....ccccaggccttcaccacca 1001

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	291	29.1	409	7	CN274427 170005313
2	159.2	15.9	599	2	BB618671 BB618671
3	159.2	15.9	614	2	BB651920 BB651920
4	154.8	15.5	649	6	CF531069 UI-M-FY0-
5	154.8	15.5	688	6	CF531121 UI-M-FY0-
6	129.6	12.9	1523	10	AG448267 Mus muscu
7	127.2	12.7	1674	10	CL078342 CH216-149
8	127	12.7	1299	10	AG039481 Pan trogl
9	126.8	12.7	1690	10	AG435238 Mus muscu
10	126.2	12.6	1692	10	AG396765 Mus muscu
11	125.4	12.5	1661	10	AG435089 Mus muscu
12	125	12.5	1961	10	AG435522 Mus muscu
13	124.2	12.4	1168	3	BM468388 AGENCOURT
14	124.2	12.4	1552	10	AG430101 Mus muscu
15	124.2	12.4	1822	10	AG435170 Mus muscu
16	123.2	12.3	1355	10	AG429718 Mus muscu
17	121.6	12.1	1425	10	AG441757 Mus muscu
18	121	12.1	1628	10	CG757066 P052-2-A0
19	120	12.1	2243	10	AG381986 Mus muscu
20	120.8	12.1	1381	10	AG396965 Mus muscu
21	119.8	12.0	1218	10	CL081011 CH216-160
22	119.8	12.0	1302	10	AG448240 Mus muscu

C 23	119.8	12.0	1400	10	AG429585	Mus muscu
C 24	119.8	12.0	1648	10	AG390465	Mus muscu
C 25	119.4	11.9	1096	5	BUB38702	AGENCOURT
C 26	119.2	11.9	1031	5	BUL167290	AGENCOURT
C 27	119	11.9	1713	10	AG435689	Mus muscu
C 28	118.6	11.8	1798	10	AG171124	Pan trogl
C 29	118.4	11.8	1288	5	BQ678719	AGENCOURT
C 30	118	11.8	1406	10	AG441598	Mus muscu
C 31	117.8	11.8	931	7	CK412737	AUF IpG11
C 32	117.6	11.6	1392	10	AG390642	Mus muscu
C 33	116.4	11.6	1286	10	AG448422	Mus muscu
C 34	116.4	11.6	1713	10	AG435689	Mus muscu
C 35	116.2	11.6	2017	10	AG435283	Mus muscu
C 36	116	11.6	1341	10	AG030611	Pan trogl
C 37	116	11.6	1403	9	CC290252	CH261-172
C 38	115.8	11.6	1449	3	BM912953	AGENCOURT
C 39	115.2	11.5	1081	10	CL464716	SAIL-1225
C 40	115.2	11.5	1785	9	CC219595	CH261-62D
C 41	115	11.5	1212	3	BQ069498	AGENCOURT
C 42	115	11.5	1453	8	DN806685	76982446
C 43	114.6	11.4	1675	10	AG360980	Mus muscu
C 44	114.6	11.4	1694	10	CL509291	SAIL-811
C 45	114.4	11.4	1454	10	AG290167	Mus muscu

## ALIGNMENTS

RESULT 1  
CN274427  
LOCUS CN274427 409 bp mRNA linear EST 16-MAY-2004  
DEFINITION 17000531326763 GRN\_ES Homo sapiens cDNA 5', mRNA sequence.  
ACCESSION CN274427  
VERSION CN274427.1 GI:47290841  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 409)  
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,  
Lebkowski, J. and Stanton, L.W.  
TITLE Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)  
PUBMED 15146197  
COMMENT Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
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FEATURES  
source  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cells, cell lines H1, H7, and H9"  
/clone\_lib="GRN\_ES"  
/note="oligo dt primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

## ORIGIN

Query Match 29.1%; Score 291; DB 7; Length 409;  
Best Local Similarity 98.1%; Pred. No. 7.4e-41;  
Matches 305; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
Query Match 29.1%; Score 291; DB 7; Length 409;  
Best Local Similarity 98.1%; Pred. No. 7.4e-41;  
Matches 305; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy	464	GCCTCTCTCTCGCGCGCGAGTTTTCAGGACAGCGCTGCGTCTCTGTCGCGCACGTGGGAAGC	523
Db	1	GGCTCTCTCTCGCGCGCGAGTTT-AGGCAGCGCTGCGTCTCTGTCGCGCACGTGGGAAGC	59
Qy	524	CCTGGCCCCGGGCGACACCCCGCGGATGCGCGCGGCTCCCGGTGCGAGCCGTGCGTCCCT	583
Db	60	CCTGGCCCCGGGCGACACCCCGCGGATGCGCGCGCTCCCGGTGCGAGCCGTGCGTCCCT	119
Qy	584	GCTGGGAGCCATACCGCGAGGTGCTGCGGTGGCGCAGTTTCGTGCGGCGGCTGGGGCC	643
Db	120	GCTGGGAGCCATACCGCGAGGTGCTGCGGTGGCGCAGTTTCGTGCGGCGGCTGGGGCC	179
Qy	644	CCAGGGCTGGCGGCTGTGTGACGCGGGGACCCCGCGGCTTTTCGCGCGCTGCTGGGCCA	703
Db	180	CCAGGGCTGGCGGCTGTGTGACGCGGGGACCCCGCGGCTTTTCGCGCGCTGCTGGGCCA	239
Qy	704	GTGCTGTGTGCGTGGCCCTGGGACGACGCGCGCCCGCGCGCCCTCTCTTCGCGCA	763
Db	240	GTGCTGTGTGCGTGGCCCTGGGACGACGCGCGCCCGCGCGCCCTCTCTTCGCGCA	299
Qy	764	GGTGGGCTCC	774
Db	300	GGTGTCTGGC	310

RESULT 2					
BB618671					
LOCUS	BB618671	599 bp	mRNA	linear	EST 26-OCT-2001
DEFINITION	BB618671	RIKEN full-length enriched, 8 days embryo Mus musculus cDNA clone 5730412M20 5', mRNA sequence.			

SOURCE	MUS MUSCULUS (house mouse)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Murinae; Mus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

#### REFERENCE AUTHORS

1 (bases 1 to 614)  
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Iehi, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sugano, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, P., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
Unpublished (2001)

#### TITLE JOURNAL COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suihito-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9226  
Fax: 81-45-503-9216  
Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)  
Wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.  
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.  
e mouse tissues.

#### FEATURES source

Location/Qualifiers  
1. .614  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="CS7BL/6J"  
/db\_xref="taxon:10090"  
/clone="C330020G14"  
/cell\_type="ES cells"  
/lab\_host="SOLR"  
/clone\_lib="RIKEN full-length enriched, ES cells"  
/note="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'  
GAGAGAGAGATTCGAGTGAATTAATTAATTCCTCCCGCCCCCCC 3']".

#### ORIGIN

Query Match 15.9%; Score 159.2; DB 2; Length 614;

Best Local Similarity 73.6%; Pred. No. 6.7e-18;  
Matches 203; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 492 CAGCGCTCGCTCCCTGCTGGCAGCGTGGAGAGCCCTGGCCCGCCACCCCGCGATGCGG 551  
Db 61 CACCTTTCGATCTTTGGTTCCCGCAGCGTGGAGAGCCCATCCCGGCTTTGAGCACATGACC 120  
Qy 552 CGCGCTCCCGCTCCCGAGCGCGTCCGCTCCCTGCTGGCGCAGCCACTACCGCGAGGTGCTG 611  
Db 121 CGCGCTCTCTGTTGCCCGCGGTGGCTCTCTGCTGGCGAGCCGATACCGGAGGTGG 180  
Qy 612 CGCGTGGCCAGTTCGTGGCGCGCTGGCGGCCCGAGGGCTGGCGGCTGGTGCAGGCGGG 671  
Db 181 CGCGTGGCAACTTTGTGGCGCGCTGGCGGCCCGAGGCGCAGCGGCTTGTGCAACCGGG 240  
Qy 672 GACCGCGCGGCTTTCGCGCGCTGGCTGGCGGCCCGAGTGGTGGTGGTGGTGGTGGTGG 731  
Db 241 GACCGGAGATCTACCGGCACTTTGTGGTGGCCCATGCTTAGTGTGATGCACTGGGGCTCA 300  
Qy 732 CGCGCGCGCCCGCGCGCCCTCCCTCCCGCAGGTG 767  
Db 301 CAGCTCCACCTCGCGACCTTCTCTCCACCGGTG 336

#### RESULT 4

CF531069  
LOCUS  
DEFINITION  
UI-M-FY0-cgp-c-19-0-UI.r1 NIH\_BMAP\_FY0 Mus musculus cDNA clone  
IMAGE:30355746 5', mRNA sequence.

#### ACCESSION

CF531069

#### VERSION

CF531069.1 GI:34583033

#### KEYWORDS

EST.

#### SOURCE

Mus musculus (house mouse)

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

#### REFERENCE

1 (bases 1 to 649)  
NIH-MSC <http://mgc.nci.nih.gov/>.

#### AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

#### TITLE

Unpublished (1999)

#### JOURNAL

Contact: Robert Strausberg, Ph.D.

#### COMMENT

Tissue Procurement: Dr. Jim Lin, University of Iowa  
Email: cgsabbs-remail.nih.gov  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mousef1.html>  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

#### FEATURES

Location/Qualifiers

1. .649  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="CS7BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30355746"  
/tissue\_type="whole brain"  
/dev\_stage="embryo 13.5, 14.5, 16.5, 17.5dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH\_BMAP\_FY0"  
/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, *Genome Research*, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail

is AGCAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

```

ORIGIN
Query Match      15.5%; Score 154.8; DB 6; Length 649;
Best Local Similarity 78.2%; Pred. No. 3.9e-17;
Matches 186; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 530 CCAGGACACCCCGGAGTCCCGGCTCCCGGTCGCGAGCGTGCCTCCCTGCTGCG 589
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Db 26 CCCGCGCTTGAGCAATGACCCGCGCTCCTCGTTGCCCGCGTGCCTCTCTGCTGCG 85
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QY 590 CAGCCACTACCGGAGGTGCTCGCGTGGCCACGCTTGTGCGGCGCTGGGCCCCAGGG 649
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Db 86 CAGCCGATACCGGAGGTGCGCGCTGGCAACCTTTGTGCGGCGCTGGGCCCCAGGG 145
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QY 650 CTGCGCGCTGTCAGCGCGGAGACCGCGGCTTTCCGCGCGTGTGTCGCCACAGTGCCT 709
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Db 146 CAGCGCGCTTGTGCAACCCGGGACCCGAGATCTACCGACCTTTGTTGCCCAATGCCT 205
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QY 710 GGTGTGCTGCTCCCTGGAGACGACGCGCGCCCGCCCGCCCTTCCTTCCGCCAGGTG 767
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Db 206 AGTGTGATGACATGGGGCTCACAGCTCCACCTGCGGACCTTTCTTCCACCAAGTGTG 263

RESULT 5
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LOCUS      CF531121
DEFINITION UI-M-FYO-cgp-m-21-0-UI.r1 NIH BMAP_FYO Mus musculus cDNA clone
            IMAGE:30355988 5', mRNA sequence.
ACCESSION CF531121
VERSION    CF531121.1 GI:34583085
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 688)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgap@remail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
Seq primer: PYX-5.
FEATURES
            Location/Qualifiers
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                /lab_host="DH10B (T1 phage resistant)"
                /clone_lib="NIH BMAP_FYO"
                /note="Organ: Brain; Vector: PYX- Asc; Site 1: EcoR I;
                Site 2: Not I; The library was constructed according
                Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
                1996. Denatured RNA was size fractionated on a 1% agarose
                gel. First strand cDNA synthesis was primed with oligo-dr
                primer containing a Not I site. Double strand cDNA was

```

size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

```

ORIGIN
Query Match      15.5%; Score 154.8; DB 6; Length 688;
Best Local Similarity 78.2%; Pred. No. 3.9e-17;
Matches 186; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 530 CCAGGACACCCCGGAGTCCCGGCTCCCGGTCGCGAGCGTGCCTCCCTGCTGCG 589
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Db 63 CCCGCGCTTGAGCAATGACCCGCGCTCCTCGTTGCCCGCGTGCCTCTCTGCTGCG 122
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QY 590 CAGCCACTACCGGAGGTGCTCGCGTGGCCACGCTTGTGCGGCGCTGGGCCCCAGGG 649
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Db 123 CAGCCGATACCGGAGGTGCGCGCTGGCAACCTTTGTGCGGCGCTGGGCCCCAGGG 182
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QY 650 CTGCGCGCTGTCAGCGCGGAGACCGCGGCTTTCCGCGCGTGTGTCGCCACAGTGCCT 709
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Db 183 CAGCGCGCTTGTGCAACCCGGGACCCGAGATCTACCGACCTTTGTTGCCCAATGCCT 242
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QY 710 GGTGTGCTGCTCCCTGGAGACGACGCGCGCCCGCCCGCCCTTCCTTCCGCCAGGTG 767
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RESULT 6
AG448267/c
LOCUS      AG448267
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-332C15.TJ, genomic survey
            sequence.
ACCESSION  AG448267
VERSION     AG448267.1 GI:48091330
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus (Japanese wild mouse)
ORGANISM    Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
            Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,
            Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriaki, K. and
            Shiroishi, T.
            Contribution of Asian mouse subspecies Mus musculus molossinus to
            genomic constitution of strain C57BL/6J, as defined by BAC-end
            sequence-SNP analysis
            Genome Res. 14 (12), 2439-2447 (2004)
            15574823
REFERENCE   2 (bases 1 to 1523)
            Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
            Direct Submission
            Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou, Tsukumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
            Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institute, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : TJ
            LIBRARY
            Vector      : pBACE3.6

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R.Site 1 : BcORI
R.Site 2 : BcORI.
Location/Qualifiers
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/db_xref="taxon:57486"
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FEATURES
Source
1..1523
Query Match 12.9%; Score 129.6; DB 10; Length 1523;
Best Local Similarity 47.2%; Pred. No. 9.4e-13;
Matches 434; Conservative 0; Mismatches 479; Indels 6; Gaps 2;

QY 73 CCCAGGCGCTCCACATCATGCGCCCTCCCTCGGGTTACCCACAGCCTTAGCGCGATTGCA 132
DB 1185 CCCGCGCCCGCGCGCGCCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1126
QY 133 CTTCTCTCGGTGGGCGCTCGTGGCGTCTCTGTGACCTCTGGAGCGGAGCGCGCGG 192
DB 1125 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1066
QY 193 GCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 252
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CH216-149D22, genomic survey sequence.
VERSION CL078342
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SOURCE GSS.
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Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 1674)
AUTHORS Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
TITLE A physical map of the xenopus tropicalis genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGTGACACTATAG
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High quality sequence start: 300
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Location/Qualifiers
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BAC library"

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Best Local Similarity 47.3%; Pred. No. 2.4e-12;
Matches 473; Conservative 0; Mismatches 522; Indels 5; Gaps 3;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

# REFERENCE AUTHORS

1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriawaki, K. and Shiroishi, T.

Contribution of Asian mouse subspecies *Mus musculus molossinus* to genomic constitution of strain C57BL/6J, as defined by BAC-end

# JOURNAL PUBMED

Genome Res. 14 (12), 2439-2447 (2004)

# REFERENCE AUTHORS

2 (bases 1 to 1692)

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

# TITLE JOURNAL

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

Teukuba Institute, Bio Resource Center,

The Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199

e-mail: abe@rtc.riken.jp

PRIMERS

Sequencing : TJ

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

# FEATURES source

Location/Qualifiers

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Matches 433; Conservative 0; Mismatches 485; Indels 3; Gaps 2;

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Qy 320 TGGGGACCCGGGACCCGCTCTCTGCGCTTCACTTCAGCTCGCCCTCTCGCGCGGAC 379

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Qy 500 CGTCTGCTCGCAGCAGCTGGGAAGCCCTTGGCCCGCGGCACCCCGCGATGCGGCGCTGCC 559

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AG435089/c

LOCUS

DEFINITION

Mus musculus molossinus DNA, clone:MSMg01-313A16.TJ, genomic survey

sequence.

ACCESSION

AG435089

VERSION

AG435089.1 GI:48078152

KEYWORDS

GSS.

SOURCE

ORGANISM

Mus musculus molossinus (Japanese wild mouse)

Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1

REFERENCE

AUTHORS

Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,

Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriawaki, K. and

Shiroishi, T.

TITLE

Contribution of Asian mouse subspecies *Mus musculus molossinus* to

genomic constitution of strain C57BL/6J, as defined by BAC-end

sequence-SNP analysis

Genome Res. 14 (12), 2439-2447 (2004)

JOURNAL

PUBMED

15574823

REFERENCE

2 (bases 1 to 1661)

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Direct Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

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(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,

Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC

library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

<b>Takuba Institute, Bio Resource Center,</b>					
<b>The Institute of Physical and Chemical Research (RIKEN) 3-1-1</b>					
<b>Koyadai, Tsukuba, 305-0074 Japan</b>					
<b>phone: 81-298-36-9189, fax: 81-298-36-9199</b>					
<b>e-mail: abe@rtc.riken.jp</b>					
<b>PRIMERS</b>					
<b>Sequencing : TJ</b>					
<b>LIBRARY</b>					
<b>Vector : pBACE3.6</b>					
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<b>R.Site 2 : ECGRI.</b>					
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Qy	179	GCGNCGCGCGCGCGGGGGAGCGGGGCCACAGCCCGCG-GTCGCGCCGGAGCACT	237		
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Qy	716	CGTGCCCTTGGGACGACGCGCGCCCCCGCGCGCCCCCTCTCTTCGCGCAGGTGGGCTGCC	775		





AUTHORS Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T., Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and Shiroishi,T.

TITLE Contribution of Asian mouse subspecies *Mus musculus molossinus* to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis

JOURNAL Genome Res. 14 (12), 2439-2447 (2004)

PUBMED 15574823

REFERENCE 2 (bases 1 to 1822)

AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

TITLE Direct Submission

JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@psc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Taububa Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp

PRIMERS

Sequencing : TJ

LIBRARY Vector : pBACe3.6

AUTHORS R.Site 1 : ECoRI.

TITLE R.Site 2 : ECoRI.

JOURNAL Location/Qualifiers

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Best Local Similarity 46.2%; Pred. No. 8.1e-12;

Matches 400; Conservative 0; Mismatches 456; Indels 10; Gaps 3;

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Qy 236 CTGCGCTGTTCGGGCGCAGGCGCGGCTCCAGTGGATTGCGGGGCACAGACCCCGAGACC 295

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Qy 296 GCGCTTCCAGTGGCGGAGGAGCTGGGGACCGGGGACCGGTCTGTCCTTCACTTC 355

Db 1118 CCGCGCGCCCCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1061

Qy 356 CAGCTCGCGCTCTCCGCGCGGACCGCGCGCGCTCCGACCCCTCCGGGTCCCGCGGCC 415

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Qy 536 CACCCCGCGATGCGCGCGCTCCCGCTCCCGAGCGTGGCTCCCTGTGCGCAGCCA 595

Db 880 CCCCCCGCC---CCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 825

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Db 588 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 529

Qy 896 CGAGTGTGCGAGAGGCTGTGCGAGCG 921

Db 528 CCNTCCNCGGGGGGGGGGGGG 503

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Job time : 4714 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 11:12:13 ; Search time 210.333 Seconds  
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3469.703 Million cell updates/sec

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Perfect score: 1001

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Gapop 10.0 , Gapext 1.0

Searched: 4637633 seqs, 364532575 residues

Total number of hits satisfying chosen parameters: 9275266

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	259.4	25.9	261	6	US-10-863-093-24
C 5	259.4	25.9	295	6	US-10-140-776A-4
C 6	259.4	25.9	295	6	US-10-140-776A-5
C 7	259.4	25.9	5928	6	US-10-863-093-25
C 8	247	24.7	2038	7	US-11-066-480-9
C 9	244	24.4	245	7	US-11-066-480-3
C 10	242.2	24.2	2041	7	US-11-066-480-11
C 11	78	7.8	78	6	US-10-863-093-7
C 12	74.2	7.4	170995	7	US-11-121-086-35
C 13	69.6	7.0	153376	7	US-11-121-086-5
C 14	68.6	6.9	268685	6	US-10-933-025-22
C 15	67.4	6.7	1557	7	US-10-996-217A-6
C 16	67	6.7	5679	7	US-11-075-185-36
C 17	67	6.7	78869	7	US-11-075-185-1
C 18	67	6.7	191684	7	US-11-121-086-2
C 19	64.8	6.5	180654	7	US-11-121-086-58
C 20	64.2	6.4	2562	7	US-11-052-554A-533
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C 22	64	6.4	171936	6	US-10-933-025-24
C 23	64	6.4	220895	6	US-10-775-169-88

C 24	63.4	6.3	191684	7	US-11-121-086-2	Sequence 2, Appli
C 25	63	6.3	26000	6	US-10-949-720-391	Sequence 391, App
C 26	62	6.2	46752	6	US-10-995-561-13410	Sequence 13410, A
C 27	62	6.2	415117	6	US-10-995-561-13274	Sequence 13274, A
C 28	60.6	6.1	150468	7	US-11-112-908-56	Sequence 56, Appl
C 29	60.6	6.1	193789	7	US-11-112-908-55	Sequence 55, Appl
C 30	60.4	6.0	2750	6	US-10-131-826A-85	Sequence 85, Appl
C 31	60.4	6.0	5706	7	US-11-052-554A-519	Sequence 519, App
C 32	59.4	5.9	150481	7	US-11-112-908-37	Sequence 37, Appl
C 33	59.4	5.9	171162	7	US-11-112-908-38	Sequence 38, Appl
C 34	59.4	5.9	1080000	6	US-10-928-446A-1	Sequence 1, Appli
C 35	59.4	5.9	1080000	6	US-10-928-446A-181	Sequence 181, App
C 36	59.4	5.9	1080000	6	US-10-928-446A-185	Sequence 185, App
C 37	59.4	5.9	1080000	6	US-10-928-446A-187	Sequence 187, App
C 38	59.4	5.9	1080000	6	US-10-928-446A-189	Sequence 189, App
C 39	59.4	5.9	1080000	6	US-10-928-446A-191	Sequence 191, App
C 40	59.4	5.9	1080000	6	US-10-928-446A-193	Sequence 193, App
C 41	59.4	5.9	1080000	6	US-10-928-446A-195	Sequence 195, App
C 42	59.4	5.9	1080000	6	US-10-928-446A-197	Sequence 197, App
C 43	59.4	5.9	1080000	6	US-10-928-446A-199	Sequence 199, App
C 44	59.4	5.9	1080000	6	US-10-928-446A-201	Sequence 201, App
C 45	59.4	5.9	1080000	6	US-10-928-446A-201	Sequence 201, App

ALIGNMENTS

RESULT 1

US-11-096-622-18/c  
; Sequence 18, Application US/11096622  
; Publication No. US2005026043A1  
; GENERAL INFORMATION:  
; APPLICANT: HUNG, MIEN-CHIE  
; APPLICANT: DAY, CHI-PING  
; APPLICANT: RAY, KUN-MING  
; APPLICANT: XIE, XIAOMING  
; APPLICANT: LI, ZHENG  
; TITLE OF INVENTION: CANCER SPECIFIC PROMOTERS  
; FILE REFERENCE: UTSC:845US  
; CURRENT APPLICATION NUMBER: US/11/096,622  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: 60/559,111  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 496  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
US-11-096-622-18

Query Match 41.2%; Score 412.4; DB 7; Length 496;  
Best Local Similarity 98.4%; Pred. No. 7.1e-52;  
Matches 427; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy	92	GGCCCTCCCTCGGGTTACCCACAGCCTAGCCGATTCGACCTCTCTCCGCTGGGGCCC	151
Db	433	GGCCCTCCCTCGGGTTACCCACAGCCTAGCCGATTCGACCTCTCTCCGCTGGGGCCC	374
Qy	152	TGCTGGGGTCCCTGCGACCTCGGGAGCGCGAGCGCGGGGGAAGCGCGGCCCA	211
Db	373	TGCTGGGGTCCCTGCGACCTCGGGAGCGCGAGCGCGGGGGAAGCGCGGCCCA	314
Qy	212	GACCCCGGGTCCGCGCGAGCAGCTGCGCTGTTCGGGGCCAGCGCGGGCTCCCACTGGAT	271
Db	313	GACCCCGGGTCCGCGCGAGCAGCTGCGCTGTTCGGGGCCAGCGCGGGCTCCCACTGGAT	254
Qy	272	TGCGGGGACAGAGCGCCGAGACCGCGCTTCCCACTGGGGAGGGAATGGGGACCCGGG	331
Db	253	TGCGGGGACAGAGCGCCGAGACCGCGCTTCCCACTGGGGAGGGAATGGGGACCCGGG	194

QY 332 CACCGCTCCGCGGCTTACCTTCCAGCTCCGCTCCGCTCCGCGGAGACCCGCGCGTCC 391  
Db 193 CACCGCTCCGCGGCTTACCTTCCAGCTCCGCTCCGCTCCGCGGAGACCCGCGCGTCC 134  
QY 392 CGACCCCTCCCGGGTCCCGGCGCCAGCCCTCCGCGGCTCCAGCCCTCCCGCTTCCCT 451  
Db 133 CGACCCCTCCCGGGTCCCGGCGCCAGCCCTCCGCGG-CTTCCAGCCCGCCCTTCCCT 75  
QY 452 TTCCGCGGCGCGGCTTCTCTCCGCGGCGAGTTTTCAGGCGAGCTGCTGCTGCG 511  
Db 74 TTCCGCGGCGCGGCTTCTCTCCGCGGCGAGTTTTCAGGCGAGCTGCTGCTGCTGCG 15  
QY 512 CACGTGGGAAGCCC 525  
Db 14 CACGTGGGCGGCCC 1  
RESULT 2  
US-11-096-622-21/c  
; Sequence 21, Application US/11096622  
; Publication No. US20050260643A1  
; GENERAL INFORMATION:  
; APPLICANT: HUNG, MIEN-CHIE  
; APPLICANT: DAY, CHI-PING  
; APPLICANT: RAU, KUN-MING  
; APPLICANT: XIE, XIAOMING  
; APPLICANT: LI, ZHENG  
; TITLE OF INVENTION: CANCER SPECIFIC PROMOTERS  
; FILE REFERENCE: UTSC:845US  
; CURRENT APPLICATION NUMBER: US/11/096,622  
; PRIOR FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: 60/559,111  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 8565  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
US-11-096-622-21  
Query Match 41.2%; Score 412.4; DB 7; Length 8565;  
Best Local Similarity 98.4%; Pred. No. 3.5e-52;  
Matches 427; Conservative 0; Mismatches 6; Indels 1; Gaps 1;  
QY 92 GGCCCTCCCTCGGGTTACCCACAGCTAGCCGATTCGACCTCTCTCCGCTGGGGCCC 151  
Db 1772 GGCCCTCCCTCGGGTTACCCACAGCTAGCCGATTCGACCTCTCTCCGCTGGGGCCC 1713  
QY 152 TCCTGCGGCTCCCTGACCTTCGAGCGCGAGCGCGCGGGGAGCGGCGCCCA 211  
Db 1712 TCCTGCGGCTCCCTGACCTTCGAGCGCGAGCGCGCGGGGAGCGGCGCCCA 1653  
QY 212 GACCCCGGGTCCGCGGAGCAGCTGCTGTTCGGGGCCAGCGCGGCTCCCAAGTGAT 271  
Db 1652 GACCCCGGGTCCGCGGAGCAGCTGCTGTTCGGGGCCAGCGCGGCTCCCAAGTGAT 1593  
QY 272 TCGGGGGACAGACGCCCGGAGACCGCTTCCGAGCTGGCGGAGGAGCTGGGGACCGGG 331  
Db 1592 TCGGGGGACAGACGCCCGGAGACCGCTTCCGAGCTGGCGGAGGAGCTGGGGACCGGG 1533  
QY 332 CACCGCTCCTGCCCTTTCACCTTCCAGCTCCGCTCCGCTCCGCGGAGACCCGCGCTCC 391  
Db 1532 CACCGCTCCTGCCCTTTCACCTTCCAGCTCCGCTCCGCTCCGCGGAGACCCGCGCTCC 1473  
QY 392 CGACCCCTCCCGGGTCCCGGCGCCAGCCCTTCGCGGCGCTTCCAGCCCTTCCCTTCT 451  
Db 1472 CGACCCCTCCCGGGTCCCGGCGCCAGCCCTTCCGCGG-CTTCCAGCCCGCCCTTCTCT 1414

QY 452 TTCCGCGGCGCGGCTTCTCTCCGCGGCGAGTTTTCAGGCGAGCTGCTGCTGCTGCG 511  
Db 1413 TTCCGCGGCGCGGCTTCTCTCTCCGCGGCGAGTTTTCAGGCGAGCTGCTGCTGCTGCG 1354  
QY 512 CACGTGGGAAGCCC 525  
Db 1353 CACGTGGGCGGCCC 1340  
RESULT 3  
US-11-066-480-2  
; Sequence 2, Application US/11066480  
; Publication No. US20050282280A1  
; GENERAL INFORMATION:  
; APPLICANT: ENNIST, DAVID LEONARD  
; TITLE OF INVENTION: ONCOLYTIC ADENOVIRAL ENCODING GM-CSF  
; FILE REFERENCE: GTIN-001  
; CURRENT APPLICATION NUMBER: US/11/066,480  
; CURRENT FILING DATE: 2005-02-28  
; PRIOR APPLICATION NUMBER: US/10/925,205  
; PRIOR FILING DATE: 2004-08-23  
; PRIOR APPLICATION NUMBER: 60/499,312  
; PRIOR FILING DATE: 2003-08-28  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 397  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-066-480-2  
Query Match 39.7%; Score 397; DB 7; Length 397;  
Best Local Similarity 100.0%; Pred. No. 1.2e-49;  
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 149 CCTTCGCTGCGTCCCTGACACCTCTGGGAGCGCAGCGCGCGGGGAGCGCGGC 208  
Db 1 CCTTCGCTGCGTCCCTGACACCTCTGGGAGCGCAGCGCGCGGGGAGCGCGGC 60  
QY 209 CCAGACCCCGGGTCCCGCGGAGCAGCTGCTGTTCGGGGCCAGGCGCGGCTCCCAAGTG 268  
Db 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCTGTTCGGGGCCAGGCGCGGCTCCCAAGTG 120  
QY 269 GATTTCGGGGCACAGACCGCCAGACCGCTTCCACGCTGGCGGAGGAGCTGGGGACCC 328  
Db 121 GATTTCGGGGCACAGACCGCCAGACCGCTTCCACGCTGGCGGAGGAGCTGGGGACCC 180  
QY 329 GGGCACCCGCTCCGCGGCTTTCACCTTCAGCTCCGCTCCCTCCGCGGAGACCCGCGCG 388  
Db 181 GGGCACCCGCTCCGCGGCTTTCACCTTCAGCTCCGCTCCCTCCGCGGAGACCCGCGCG 240  
QY 389 TCCGACCCCTTCGCGGCTCCCGGCGCCAGCCCTTCCTCCGCGGCTTCCTCCAGCCCTTCCCTTT 448  
Db 241 TCCGACCCCTTCGCGGCTCCCGGCGCCAGCCCTTCCTCCGCGGCTTCCTCCAGCCCTTCCCTTT 300  
QY 449 CTTTTCGGGGCGCGGCTTCCTTCGCGGCGGAGTTTCAGGCGAGCTGCTGCTGCT 508  
Db 301 CTTTTCGGGGCGCGGCTTCCTTCGCGGCGGAGTTTCAGGCGAGCTGCTGCTGCT 360  
QY 509 GCGCAGCTGGGAGACCCCTTCGCGGCGGAGCTTCGCGGCGGAGCTTCGCGGCGGAGCTTCGCTGCT 545  
Db 361 GCGCAGCTGGGAGACCCCTTCGCGGCGGAGCTTCGCGGCGGAGCTTCGCGGCGGAGCTTCGCTGCT 397  
RESULT 4  
US-10-863-093-24  
; Sequence 24, Application US/10863093  
; Publication No. US20050269081A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrews, William H.  
; APPLICANT: Foster, Christopher A.  
; APPLICANT: Fraser, Stephanie  
; APPLICANT: Mohammadpour, Hamid

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; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
; TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
; FILE REFERENCE: SIER-005
; CURRENT APPLICATION NUMBER: US/10/863,093
; CURRENT FILING DATE: 2004-06-08
; PRIOR APPLICATION NUMBER: US/09/932,581
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/227,865
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/230,174
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/238,345
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 261
; TYPE: DNA
; ORGANISM: human
US-10-863-093-24

Query Match      25.9%; Score 259.4; DB 6; Length 261;
Best Local Similarity 99.6%; Pred. No. 8.5e-30;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 288 CCAGGACCGCGCTTCCACAGTGGCGGAGGAGTGGGGACCCCGGACCCGCTCTGCCCT 347
DB 1 CCAGGACCGCGCTTCCACAGTGGCGGAGGAGTGGGGACCCCGGACCCGCTCTGCCCT 60

QY 348 TCACCTTCCAGTCCGCTCTCCCGCGGAGCCCGCCGCTCCCGACCCCTCCCGGTC 407
DB 61 TCACCTTCCAGTCCGCTCTCCCGCGGAGCCCGCCGCTCCCGACCCCTCCCGGTC 120

QY 408 CCGGCGGACCCCTCCGGGCTCCAGGCGCTCCAGGCGCTCCGCTCCGCGGCGCCG 467
DB 121 CCGGCGGACCCCTCCGGGCTCCAGGCGCTCCAGGCGCTCCGCTCCGCGGCGCCG 180

QY 468 TCTCTCCGCGGCGAGTTTTCAGGCGAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTG 527
DB 181 TCTCTCCGCGGCGAGTTTTCAGGCGAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTG 240

QY 528 GCCCGGCGCACCCCGCGATG 548
DB 241 GCCCGGCGCACCCCGCGATG 261

RESULT 5
US-10-140-776A-4
; Sequence 4, Application US/10140776A
; Publication No. US20050250186A1
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Foster, Christopher
; APPLICANT: Fraser, Stephanie
; APPLICANT: Mohammadpour, Hamid
; TITLE OF INVENTION: Methods and Compositions for Modulating
; TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Expression
; FILE REFERENCE: SIER-013
; CURRENT APPLICATION NUMBER: US/10/140,776A
; CURRENT FILING DATE: 2202-05-07
; PRIOR APPLICATION NUMBER: 60/289,717
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 295
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-140-776A-4

Query Match      25.9%; Score 259.4; DB 6; Length 295;
Best Local Similarity 97.8%; Pred. No. 8.2e-30;
Matches 263; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 288 CCAGGACCGCGCTTCCACAGTGGCGGAGGAGTGGGGACCCCGGACCCGCTCTGCCCT 347
DB 23 CCAGGACCGCGCTTCCACAGTGGCGGAGGAGTGGGGACCCCGGACCCGCTCTGCCCT 82

QY 348 TCACCTTCCAGTCCGCTCTCCCGCGGAGCCCGCCGCTCCCGACCCCTCCCGGTC 407
DB 83 TCACCTTCCAGTCCGCTCTCCCGCGGAGCCCGCCGCTCCCGACCCCTCCCGGTC 142

QY 408 CCGGCGGACCCCTCCGGGCTCCAGGCGCTCCAGGCGCTCCGCTCCGCGGCGCCG 467
DB 143 CCGGCGGACCCCTCCGGGCTCCAGGCGCTCCAGGCGCTCCGCTCCGCGGCGCCG 202

QY 468 TCTCTCCGCGGCGAGTTTTCAGGCGAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTG 527
DB 203 TCTCTCCGCGGCGAGTTTTCAGGCGAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTG 262

QY 528 GCCCGGCGCACCCCGCGATG 548
DB 263 GCCCGGCGCACCCCGCGATG 291

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Best Local Similarity 97.8%; Pred. No. 8.2e-30;
Matches 263; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 288 CCAGGACCGCGCTTCCACAGTGGCGGAGGAGTGGGGACCCCGGACCCGCTCTGCCCT 347
DB 23 CCAGGACCGCGCTTCCACAGTGGCGGAGGAGTGGGGACCCCGGACCCGCTCTGCCCT 82

QY 348 TCACCTTCCAGTCCGCTCTCCCGCGGAGCCCGCCGCTCCCGACCCCTCCCGGTC 407
DB 83 TCACCTTCCAGTCCGCTCTCCCGCGGAGCCCGCCGCTCCCGACCCCTCCCGGTC 142

QY 408 CCGGCGGACCCCTCCGGGCTCCAGGCGCTCCAGGCGCTCCGCTCCGCGGCGCCG 467
DB 143 CCGGCGGACCCCTCCGGGCTCCAGGCGCTCCAGGCGCTCCGCTCCGCGGCGCCG 202

QY 468 TCTCTCCGCGGCGAGTTTTCAGGCGAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTG 527
DB 203 TCTCTCCGCGGCGAGTTTTCAGGCGAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTG 262

QY 528 GCCCGGCGCACCCCGCGATG 548
DB 263 GCCCGGCGCACCCCGCGATG 291

RESULT 6
US-10-140-776A-5
; Sequence 5, Application US/10140776A
; Publication No. US20050250186A1
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Foster, Christopher
; APPLICANT: Fraser, Stephanie
; APPLICANT: Mohammadpour, Hamid
; TITLE OF INVENTION: Methods and Compositions for Modulating
; TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Expression
; FILE REFERENCE: SIER-013
; CURRENT APPLICATION NUMBER: US/10/140,776A
; CURRENT FILING DATE: 2202-05-07
; PRIOR APPLICATION NUMBER: 60/289,717
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 295
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-140-776A-5

Query Match      25.9%; Score 259.4; DB 6; Length 295;
Best Local Similarity 97.8%; Pred. No. 8.2e-30;
Matches 263; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 288 CCAGGACCGCGCTTCCACAGTGGCGGAGGAGTGGGGACCCCGGACCCGCTCTGCCCT 347
DB 23 CCAGGACCGCGCTTCCACAGTGGCGGAGGAGTGGGGACCCCGGACCCGCTCTGCCCT 82

QY 348 TCACCTTCCAGTCCGCTCTCCCGCGGAGCCCGCCGCTCCCGACCCCTCCCGGTC 407
DB 83 TCACCTTCCAGTCCGCTCTCCCGCGGAGCCCGCCGCTCCCGACCCCTCCCGGTC 142

QY 408 CCGGCGGACCCCTCCGGGCTCCAGGCGCTCCAGGCGCTCCGCTCCGCGGCGCCG 467
DB 143 CCGGCGGACCCCTCCGGGCTCCAGGCGCTCCAGGCGCTCCGCTCCGCGGCGCCG 202

QY 468 TCTCTCCGCGGCGAGTTTTCAGGCGAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTG 527
DB 203 TCTCTCCGCGGCGAGTTTTCAGGCGAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTG 262

QY 528 GCCCGGCGCACCCCGCGATG 548
DB 263 GCCCGGCGCACCCCGCGATG 291

```

## RESULT 7

US-10-863-093-25  
; Sequence 25, Application US/10863093  
; Publication No. US20050269081A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrews, William H.  
; APPLICANT: Foster, Christopher A.  
; APPLICANT: Fraser, Stephanie  
; APPLICANT: Mohammadpour, Hamid  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING  
; FILE REFERENCE: SIER-005  
; CURRENT APPLICATION NUMBER: US/10/863,093  
; CURRENT FILING DATE: 2004-06-08  
; PRIOR APPLICATION NUMBER: US/09/932,581  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/227,865  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: 60/230,174  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/238,345  
; PRIOR FILING DATE: 2000-10-05  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 5928  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic expression plasmid  
US-10-863-093-25

Query Match 25.9%; Score 259.4; DB 6; Length 5928;  
Best Local Similarity 97.8%; Pred. No. 3.9e-30;  
Matches 263; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 288 CCAGACCGCGCTCCACAGTGGGGAGGAGTGGGACCCGGGACCCGCTCTCGCCCT 347  
Db 38 CCAGACCGCGCTCCACAGTGGGGAGGAGTGGGACCCGGGACCCGCTCTCGCCCT 97  
Qy 348 TCACCTTCAGCTCGCGCTCTCCGCGGACCCCGCGCTCCGACCCCTCCGGGTC 407  
Db 98 TCACCTTCAGCTCGCGCTCTCCGCGGACCCCGCGCTCCGACCCCTCCGGGTC 157  
Qy 408 CCGCGCCAGCCCTCCGCGGCTCCAGCCCTCCAGCCCTCCCTTCCTTCGCGGCCCCGCC 467  
Db 158 CCGCGCCAGCCCTCCGCGGCTCCAGCCCTCCAGCCCTCCCTTCCTTCGCGGCCCCGCC 217  
Qy 468 TCTCTCGCGGCGAGTTTCAGGACGCTGCGTCTGTCGCGACGTGGGAAGCCCTG 527  
Db 218 TCTCTCGCGGCGAGTTTCAGGACGCTGCGTCTGTCGCGACGTGGGAAGCCCTG 277  
Qy 528 GCCCGGCGACCCCGCGATCGCGGC 556  
Db 278 GCCCGGCGACCCCGCGATTCGCCAC 306

## RESULT 8

US-11-066-480-9  
; Sequence 9, Application US/11066480  
; Publication No. US2005028280A1  
; GENERAL INFORMATION:  
; APPLICANT: ENNIST, DAVID LEONARD  
; TITLE OF INVENTION: ONCOLYTIC ADENOVIRAL ENCODING GM-CSF  
; FILE REFERENCE: GTIN-001  
; CURRENT APPLICATION NUMBER: US/11/066,480  
; CURRENT FILING DATE: 2005-02-28  
; PRIOR APPLICATION NUMBER: US/10/925,205  
; PRIOR FILING DATE: 2004-08-23  
; PRIOR APPLICATION NUMBER: 60/499,312  
; PRIOR FILING DATE: 2003-08-28

; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9

; LENGTH: 2038  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: 1 to 2038 of Ar20-1006 including an ITR, packaging signal, poly A  
; OTHER INFORMATION: , hTERT promoter, Ela gene and a portion of the Elb gene.  
US-11-066-480-9

Query Match 24.7%; Score 247; DB 7; Length 2038;  
Best Local Similarity 96.2%; Pred. No. 3.1e-28;  
Matches 253; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 284 AGCCCCAGGACCGCGCTTCCACGTGGCGGAGGAGTGGGACCCGGGACCCGCTCTGC 343  
Db 529 ATGTCTGATCCGCTAGCCCACTGGCGGAGGAGTGGGACCCGGGACCCGCTCTGC 588  
Qy 344 CCCTTCACCTTCCAGCTCCGCTCCTCGCGGAGGACCCCGCGCTCCGACCCCTCCG 403  
Db 589 CCCTTCACCTTCCAGCTCCGCTCCTCGCGGAGGACCCCGCGCTCCGACCCCTCCG 648  
Qy 404 GGTCCCGGCGGACCCCTCCGCGGCTCCAGCCCTCCCTTCCTTCCTTCGCGGCCCC 463  
Db 649 GGTCCCGGCGGACCCCTCCGCGGCTCCAGCCCTCCCTTCCTTCCTTCGCGGCCCC 708  
Qy 464 GCCCTCTCTCGCGGCGGAGTTTCAGGACGCTGCTGCTGCGACGTGGGAAGC 523  
Db 709 GCCCTCTCTCGCGGCGGAGTTTCAGGACGCTGCTGCTGCGACGTGGGAAGC 768  
Qy 524 CCTGGCCCGGCGCACCCCGCGA 546  
Db 769 CCTGGCCCGGCGCACCCCGCGA 791

## RESULT 9

US-11-066-480-3  
; Sequence 3, Application US/11066480  
; Publication No. US2005028280A1  
; GENERAL INFORMATION:  
; APPLICANT: ENNIST, DAVID LEONARD  
; TITLE OF INVENTION: ONCOLYTIC ADENOVIRAL ENCODING GM-CSF  
; FILE REFERENCE: GTIN-001  
; CURRENT APPLICATION NUMBER: US/11/066,480  
; CURRENT FILING DATE: 2005-02-28  
; PRIOR APPLICATION NUMBER: US/10/925,205  
; PRIOR FILING DATE: 2004-08-23  
; PRIOR APPLICATION NUMBER: 60/499,312  
; PRIOR FILING DATE: 2003-08-28  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 245  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-066-480-3

Query Match 24.4%; Score 244; DB 7; Length 245;  
Best Local Similarity 100.0%; Pred. No. 1.4e-27;  
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CCCACGTGGCGGAGGAGTGGGACCCGGGACCCGCTTCCTGCGCCCTTCCAGCTC 361  
Db 2 CCCACGTGGCGGAGGAGTGGGACCCGGGACCCGCTTCCTGCGCCCTTCCAGCTC 61  
Qy 362 CGCCTCTCTCGCGGAGGAGTGGGACCCGCTTCCTGCGGCTCCCGGCCCCAGGCCCC 421  
Db 62 CGCCTCTCTCGCGGAGGAGTGGGACCCGCTTCCTGCGGCTCCCGGCCCCAGGCCCC 121  
Qy 422 CTCGCGGCGCTTCCAGCCCTTCCTTCCTTCCTTCGCGGCCCCGCGCTCTCTCGGCGC 481  
Db 122 CTCGCGGCGCTTCCAGCCCTTCCTTCCTTCCTTCGCGGCCCCGCGCTCTCTCGGCGC 181

Qy	482	GAGTTTCAGGCAGCGCTCGTCTGCTGCGCAGCTGGCGAGCCCTGGCCCCCGGCCACCCC	541
Db	182	GAGTTTCAGGCAGCGCTCGTCTGCTGCGCAGCTGGCGAGCCCTGGCCCCCGGCCACCCC	241
Qy	542	CGCG	545
Db	242	CGCG	245

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RESULT 10
US-11-066-480-11
; Sequence 11, Application US/11066480
; Publication No. US20050282280A1
; GENERAL INFORMATION:
; APPLICANT: ENNST, DAVID LEONARD
; TITLE OF INVENTION: ONCOLYTIC ADENOVIRAL ENCODING GM-CSF
; FILE REFERENCE: GTIN-001
; CURRENT APPLICATION NUMBER: US/11/066,480
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/10/925,205
; PRIOR FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: 60/499,312
; PRIOR FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 2041
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: 1 to 2041 of A:20-1010, including an ITR, packaging signal, poly
; OTHER INFORMATION: A, hTERT promoter, Ela gene and a portion of the Elb gene
US-11-066-480-11

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RESULT 11  
US-10-863-093-7  
; Sequence 7, Application US/10863093  
; Publication No. US20050269081A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrews, William H.  
; APPLICANT: Foster, Christopher A.  
; APPLICANT: Fraser, Stephanie  
; APPLICANT: Mohammadpour, Hamid  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING  
; TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TEXT) EXPRESSION  
; FILE REFERENCE: SIER-005  
; CURRENT APPLICATION NUMBER: US/10/863,093

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; CURRENT FILING DATE: 2004-06-08
; PRIOR APPLICATION NUMBER: US/09/932,581
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/227,865
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/230,174
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/238,345
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 78
; TYPE: DNA
; ORGANISM: human
; US-10-863-093-7

Query Match          7.8%; Score 78; DB 6; Length 78;
Best Local Similarity 100.0%; Pred.No.0.0014;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 CTCTCTCGCGCGGAGTTTCAGGCAGCGCTGCTGCTGCGCACGTGGGAAGCCCTGG 528
Db 1 CTCTCTCGCGCGGAGTTTCAGGCAGCGCTGCTGCTGCGCACGTGGGAAGCCCTGG 60

QY 529 CCCC GGCCACCCCGCGGA 546
Db 61 CCCC GGCCACCCCGCGGA 78

RESULT 12
US-11-121-086-35/c
; Sequence 35, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 170995
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-35

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; CURRENT APPLICATION NUMBER: US/10/863,093

Db 106092 G C C C C G C T G C A T G T C T G C G C G C C C T A G C C G A G G A T G C T G A G A T G A A G C T G C C G C T G 106033  
Qy 501 G T C T G C T G C G C A C G T G G G A A G C C C T G C C C C C G C C A C C C C C G G A T G C G C G C G C T C C C 560  
Db 106032 A A G C C A A C G C A C C C C G C G A G C C C C G C C C G A G C G A G A G C C C G A G C G C G C G 105973  
Qy 561 G C T C G C G A G C C G T G C G T C C C T G C G C A G C C A C T A C C G C G A G T G C T G C C G C T G C C C 620  
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Qy 621 A C G T T C G T G C G C G C C T G G G C C C C A G G G C T G G G C G T G T G T G C A G C G G G A C C C G C G C G 680  
Db 105912 C C G C C G C G C C G T G C G C G G C C C T C T G C G C C G C C G C G C A C T G C C C C C C C C C C C C C C C G 105853  
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Qy 741 C C C C C G C C C C C T C T T C C G C C A G T G G G C C T C C C C G G G T G C G C T C C G S C T G G G G T T G 800  
Db 105792 T C G C G C G C T G C C G A G A G G C G G G T A T A C A G T G T T C G G G C T G T G T G C T G G G C T G C 105733  
Qy 801 A G G C C G C C G C G G G A A C C A G C G A C A T G C G G A G A C A G C G C A G C A C T C A G G C G C T T C 860  
Db 105732 G C G C A G C C C T G A G T T C A T G T G C - G G G C T G C T G G A C C T G T G C A C C C G C T G A G C T G C 105675  
Qy 861 C C C C G A G T G T C T G C T G A A G A G C T G T G G C C C C A G T G C T C A G A G G C T G T G C A G C 920  
Db 105674 G C T T C C T T G G C T G C T G C T G A G A C C T G G C G C G A A G G A C T A C C A C T A C C T G C G C G A C T 105615  
Qy 921 G C G C G C G A A G A C G T G C T G C C T T C G C C T T C G C G C T G C G A G C G G G C C C G C G G G G C C 980  
Db 105614 C G A G G C C A A G C C A A C A G C C C T C T C G A C C C G G G C C G C T G G C C G A C T T C G A G A G C C G 105555  
Qy 981 C 981  
Db 105554 C 105554

## RESULT 13

US-11-121-086-5  
; Sequence 5, Application US/11121086  
; Publication No. US2005026459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR FILING DATE: 2005-05-04  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5  
; LENGTH: 153376  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-121-086-5

Query Match 7.0%; Score 69.6; DB 7; Length 153376;

Best Local Similarity 45.5%; Pred. No. 0.0034;  
Matches 322; Conservative 0; Mismatches 384; Indels 2; Gaps 2;

Qy 148 G C C C T G C T G C G C C C T G C A C C C T G G A G C G C G A G C G C G C G C G - G C G C G G G A A G C G C G 206  
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Qy 207 G C C C A G A C C C C G G G T C C C C C G A G A C A G T G C G T G T G G G G C A G C C G G G C T C C A G 266  
Db 56838 G G G A G G G A A A C A A G A T G G C G C G C G T G T C G G C G C G A A G G G A G G C G C C G 56897  
Qy 267 T G G A T T C G C G G G C A C A G A C C C C A G A C C G C T T C C C A C C T G C G G A G G A C T G G G G A C 326

Db 56898 G G G C C C C G A G T A G A G C C C G G G C G C A A G A G A C C G G G T G G C G G A C T T G C T G C C 56957  
Qy 327 C C G G G C A C C C G T C C T G C C C C T T C A C C T T C A G T C C G C C T C C T C C G C G C G A C C C C G C C C 386  
Db 56958 G C G C C T T G A T G A T G G G C T G G C C C C C C C C C T C G C G C T C C G C C T C C T C C A C A C A C G C G C G C G C C 57017  
Qy 387 C G T C C C G A C C C C T C C C G G G T C C C G C C C A G C C C C C T C C G G G C C C T C C A G C C C C T C C C C 446  
Db 57018 G C G C G A G G G G A C G C G C C C C C G G G C C C G A C C T T C G G G A A C C C C C C G C C C G A G C 57077  
Qy 447 T T C T T T C C C G C C C C C G C C C T C T C T C T C G C G G C G A G T T T C A G G C A G C G T G C G T C T G 506  
Db 57078 C T G G G C C T G C G C G C C T C G C C C C G G A G C C C C G T G A G C C C C C G C G C G C C G C C 57137  
Qy 507 C T G C G C A C G T G G G A A G C C C T G G C C C C G C C A C C C C C C A T G C G C G C G T C C C C G C T G C 566  
Db 57138 C C G C G A C C G A C G C T G A G G G C A C T C G G G G C G G G C G C G C T C G G G C A G A C G T T T G C G 57197  
Qy 567 C A G C C G T G C G C C C C T G C G C A G C C A C T A C C G A G G T G C C C G C T G C C G C T G G C C A C G T T C 626  
Db 57198 G A A G G G G G C C C T G C C G G C C C C G C G A C C A C C T T G G G G G T C G C G G C C G G C T G C G G G 57257  
Qy 627 G T G C G C G C C T G G G C C C C A G G G C T G C G C G T G T G C A G C G C G C G G A C C C G - G C G G C T T T 685  
Db 57258 G C G C C A C T G C G G C C C T C C G G G C C C G G G C A G C A C A G C C C T G A G C G A G C T G T T G 57317  
Qy 686 C C G C G C C T G T G C C C A G T G C C T G T G T G C C T G G A C G C A C G C C C C C C C C C C G C 745  
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Qy 746 C G C C C C C T C T T C C C A G T G G C C C C C G G G T G C G C G T C C G G T G G G G T T G A G G G C 805  
Db 57378 A G T C G G C G C C C C C G G A G T C C G C T C G T C G C C G C G A G C G T T G C T C T G G G A C 57437  
Qy 806 G G C G G G G A A C C A G C G A C A T G C G A G A G C A G C G C A G G C G A C T C A G G 853  
Db 57438 A G C G T G G G A C C C G G G C G T C G C G G A G A C C C C C C A G C G A A G T T G G G 57485

## RESULT 14

US-10-933-025-22/c  
; Sequence 22, Application US/10933025  
; Publication No. US20050265987A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSEN, STEVEN  
; APPLICANT: HEMMERICH, STEFAN  
; APPLICANT: TOMITA, MEGUMI  
; TITLE OF INVENTION: Sulfotransferases and methods of use  
; TITLE OF INVENTION: thereof  
; FILE REFERENCE: UCAL-2300CON  
; CURRENT APPLICATION NUMBER: US/10/933,025  
; CURRENT FILING DATE: 2004-09-01  
; PRIOR APPLICATION NUMBER: 10/025,966  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/258,577  
; PRIOR FILING DATE: 2000-12-27  
; PRIOR APPLICATION NUMBER: 60/267,831  
; PRIOR FILING DATE: 2001-09-02  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 268685  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(268685)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-933-025-22

Query Match

Best Local Similarity 6.9%; Score 68.6; DB 6; Length 268685;

Matches 48.0%; Pred. No. 0.0041;



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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 10:37:31 ; Search time 949.333 Seconds  
(without alignments)  
8719.432 Million cell updates/sec

Title: US-09-615-039-1\_COPY\_13000\_14000

Perfect score: 1001

Sequence: 1 cgtccgacctggagcgc.....ccccggagccttcaccacca 1001

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
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- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1001	100.0	4321	6	US-10-325-810-6
2	1001	100.0	15418	3	US-09-783-203-1
3	1001	100.0	15418	3	US-09-994-427A-1
4	1001	100.0	15418	3	US-09-995-419A-1
5	1001	100.0	15418	5	US-10-141-220-1
6	1001	100.0	15418	5	US-10-023-969-1
7	1001	100.0	15418	5	US-10-206-447-1
8	1001	100.0	15418	7	US-10-674-836-1
9	1001	100.0	15418	7	US-10-811-012-1
10	999.4	99.8	26414	8	US-10-840-455-43
11	999.4	99.8	51552	3	US-09-733-294A-30
12	945.8	94.5	4335	8	US-10-877-124-6
13	945.8	94.5	4335	8	US-10-877-022-6
14	945.8	94.5	4335	8	US-10-877-146-6
15	926.8	92.6	4200	5	US-10-044-692-6
16	926.8	92.6	4200	5	US-10-044-539-6
17	867.6	86.7	4293	8	US-10-456-830-1
18	572.2	57.2	4356	7	US-10-240-589C-144
19	546.4	54.6	5126	8	US-10-840-455-1
20	546.4	54.6	11276	8	US-10-840-455-3
21	502.2	50.2	35871	3	US-09-956-335-2
22	502.2	50.2	35978	3	US-09-956-335-1
23	499	49.9	1677	3	US-09-956-335-3

Sequence 143, Appl  
Sequence 51, Appl  
Sequence 55, Appl  
Sequence 59, Appl  
Sequence 79, Appl  
Sequence 67, Appl  
Sequence 83, Appl  
Sequence 71, Appl  
Sequence 65, Appl  
Sequence 75, Appl  
Sequence 32, Appl  
Sequence 35, Appl  
Sequence 93, Appl  
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Sequence 6, Appl  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 8, Appl  
Sequence 17, Appl  
Sequence 9, Appl  
Sequence 8, Appl

## ALIGNMENTS

RESULT 1  
US-10-325-810-6  
; Sequence 6, Application US/10325810  
; Publication No. US20030204069A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; ; Lingner, Joachim  
; ; Nakamura, Toru  
; ; Chapman, Karen B.  
; ; Morin, Gregg B.  
; ; Harley, Calvin B.  
; ; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 633  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/325,810  
; FILING DATE: 20-Dec-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/402,181  
; FILING DATE: 29-Sep-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951

;; FILING DATE: 14-AUG-1997  
;; APPLICATION NUMBER: US 08/915,503  
;; FILING DATE: 14-AUG-1997  
;; APPLICATION NUMBER: WO PCT/US97/17885  
;; FILING DATE: 01-OCT-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Aussenhus, Scott L.  
;; REGISTRATION NUMBER: 42,271  
;; REFERENCE/DOCKET NUMBER: 015389-002620US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4321 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: -  
;; LOCATION: 1..4321  
;; OTHER INFORMATION: /note= "genomic DNA insert of pGRN14"  
;; FEATURE:  
;; NAME/KEY: intron  
;; LOCATION: 2702..2804  
;; OTHER INFORMATION: /note= "intron 1"  
;; FEATURE:  
;; NAME/KEY: intron  
;; LOCATION: 4160..4313  
;; OTHER INFORMATION: /note= "intron 2"  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-325-810-6

Query Match 100.0%; Score 1001; DB 6; Length 4321;  
Best Local Similarity 100.0%; Pred. No. 1.2e-205;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CGTCGGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCCAGCGGCAAGGGTCCCG 60  
Db 1938 CGTCGGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCCAGCGGCAAGGGTCCCG 1997  
Qy 61 CAGCACCTGTTCCAGGGCTCCACATCATATGGCCCTCCCTGGGGTTACCCACAGCCT 120  
Db 1998 CAGCACCTGTTCCAGGGCTCCACATCATATGGCCCTCCCTGGGGTTACCCACAGCCT 2057  
Qy 121 AGCCCGATTCCAGCTCTCTCGCTGGGGCCCTCGCTGGCCCTCGCTGCACCCCTGGAGCGC 180  
Db 2058 AGCCCGATTCCAGCTCTCTCGCTGGGGCCCTCGCTGGCCCTCGCTGCACCCCTGGAGCGC 2117  
Qy 181 GAGCGGCGCGGGGGAGAGCGCGGCCAGACCCCGGGTCCGCCCGGAGCAGCTGCG 240  
Db 2118 GAGCGGCGCGGGGGAGAGCGCGGCCAGACCCCGGGTCCGCCCGGAGCAGCTGCG 2177  
Qy 241 CTGTCGGGGCCAGGCCCGGGCTCCAGTGGATTCCGGGCAAGACGCCAGGACCGGCT 300  
Db 2178 CTGTCGGGGCCAGGCCCGGGCTCCAGTGGATTCCGGGCAAGACGCCAGGACCGGCT 2237  
Qy 301 TCCACACTGGCGAGGAGCTGGGACCCCGGACCCCGTCTGCTGCCCCCTTCCAGCT 360  
Db 2238 TCCACACTGGCGAGGAGCTGGGACCCCGGACCCCGTCTGCTGCCCCCTTCCAGCT 2297  
Qy 361 CCGCTCTCTCGCGGAGACCCCGCCGTCGCAACCCCTCCCGGGTCCCGGCCAGGCC 420  
Db 2298 CCGCTCTCTCGCGGAGACCCCGCCGTCGCAACCCCTCCCGGGTCCCGGCCAGGCC 2357  
Qy 421 CTTCCGGGCTCCAGCCCTCCCTTCTTTTCCGGGGCCCGCCCTCTCTCGCGGCG 480  
Db 2358 CTTCCGGGCTCCAGCCCTCCCTTCTTTTCCGGGGCCCGCCCTCTCTCGCGGCG 2417  
Qy 481 CGAGTTTCAGGACAGCTGCTCTGCTGCGCAGCTGGGAGCCCTGCGCCCGGACCC 540  
Db 2418 CGAGTTTCAGGACAGCTGCTCTGCTGCGCAGCTGGGAGCCCTGCGCCCGGACCC 2477

Qy 541 CCGCGATCCCGCGCTCCCGCTGCCGAGCGCTGGCTCCCTGCTGCGCAGCCACTACC 600  
Db 2478 CCGCGATCCCGCGCTCCCGCTGCCGAGCGCTGGCTCCCTGCTGCGCAGCCACTACC 2537  
Qy 601 GCGAGGTGCTCGCGCTGGCCACCGTTTCTGCGGGCCCTGGGGCCCCAGGGCTGGCGGCTGG 660  
Db 2538 GCGAGGTGCTCGCGCTGGCCACCGTTTCTGCGGGCCCTGGGGCCCCAGGGCTGGCGGCTGG 2597  
Qy 661 TGCAGCGCGGGGACCCCGCGGCTTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
Db 2598 TGCAGCGCGGGGACCCCGCGGCTTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2657  
Qy 721 CCTGGGAGCGACCGCGCGCCCGCGCGCCCTCTTCCGCGAGCTGGGGCTCCCGGGG 780  
Db 2658 CCTGGGAGCGACCGCGCGCCCGCGCGCCCTCTTCCGCGAGCTGGGGCTCCCGGGG 2717  
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Db 2718 TCGGCGTCCGGCTGGGGTTGAGGGCGCGCCCGGGGGAACAGCGACATGCGGAGAGCAGCG 2777  
Qy 841 CAGCGGACTCAGGGCTTCCCGCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Db 2778 CAGCGGACTCAGGGCTTCCCGCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2837  
Qy 901 GCTGCGAGGCTGTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960  
Db 2838 GCTGCGAGGCTGTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2897  
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## RESULT 2

US-09-783-203-1  
; Sequence 1, Application US/09783203  
; Patent No. US2002098582A1  
; GENERAL INFORMATION:  
; APPLICANT: Geron Corporation  
; APPLICANT: Gold, Joseph  
; APPLICANT: Lebkowski, Jane  
; TITLE OF INVENTION: Tpacked stem cells  
; FILE REFERENCE: 096/003  
; CURRENT APPLICATION NUMBER: US/09/783,203  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: 60/253,443  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/253,357  
; PRIOR FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 1  
; LENGTH: 15418  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-783-203-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 8.6e-206;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CGTCCGAGCTCGAGGAGCCCTGGGTCTCCGATCAGGCCAGCGGCAAGGGTCCCGCG 60  
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Qy 61 CAGCGACTGTTCCAGGGCTCCACATCATATGCCCCCTCCCTCGGGTTACCCACAGCCT 120  
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Qy 121 AGCCCGATTCCAGCTCTCTCTCGCTGGGGCCCTCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 180  
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QY 961 GGACGGGGCCCGGGGGGGCCCCCCCCGAGGCTTCCACCACCA 1001  
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RESULT 4

US-09-995-419A-1  
; Sequence 1, Application US/09995419A  
; Publication No. US20030032187A1  
; GENERAL INFORMATION:  
; APPLICANT: McWhir, Jim  
; APPLICANT: Gold, Joseph D.  
; APPLICANT: Schiff, J. Michael  
; TITLE OF INVENTION: 096,004 - SeqList  
; FILE REFERENCE: 096,004 - SeqList  
; CURRENT APPLICATION NUMBER: US/09/995,419A  
; CURRENT FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 60/253,357  
; PRIOR FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 15418  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-995-419A-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 8,6e-206;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCGGATCAGGCGCGGCAAGGGTCCCG 60  
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QY 241 CTGTCCGGGGCCAGCGCGGGCTCCAGTGGATTGCGGGGACAGACGCCAGGACCGCGCT 300  
Db 13240 CTGTCCGGGGCCAGCGCGGGCTCCAGTGGATTGCGGGGACAGACGCCAGGACCGCGCT 13299  
QY 301 TCCACACCTGGCGAGGACCTGGGACCCGGGACACCCGCTCTCTGCCCCCTTACCTTCCAGCT 360  
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QY 421 CCTCCGGGGCTTCCAGCCCTCCCTTCTTTCGCGGGCCCGCCCTCTCTCTCGCGCGC 480  
Db 13420 CCTCCGGGGCTTCCAGCCCTCCCTTCTTTCGCGGGCCCGCCCTCTCTCTCGCGCGC 13479  
QY 481 CGAGTTTTCAGGACAGCTGCTCTGCTGCGACAGTGGGAAGCCCTGGCCCGCCGACCC 540  
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QY 541 CCGCGATTCGCGCGCTTCCCGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACC 600  
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US-10-141-220-1  
; Sequence 1, Application US/10141220  
; Publication No. US20030040111A1  
; GENERAL INFORMATION:  
; APPLICANT: Geron Corporation  
; APPLICANT: Gold, Joseph  
; APPLICANT: Lebkowski, Jane  
; TITLE OF INVENTION: Tpacked stem cells  
; FILE REFERENCE: 096/003  
; CURRENT APPLICATION NUMBER: US/10/141,220  
; CURRENT FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: US/09/783,203  
; PRIOR FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: 60/253,443  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/253,357  
; PRIOR FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 15418  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-141-220-1

Query Match 100.0%; Score 1001; DB 5; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 8,6e-206;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCCCGATCAGGCGCAGCGCCAAAGGGTCCCG 60  
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QY 181 GAGCGCGCGGGCGGGGAAGCGCGCCAGACCCCGGGTCCCGCCGAGCAGCTGCG 240

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Db 13240 CTGTCCGGGCGCAGGCGCGGCTCCAGTGGATTTCGCGGCGCAGACGCGCCAGGACCGCGCT 13299
Qy 301 TCCACACTGCGGAGGAGCTGGGGACCCCGGACACCCGTCCTGCTGCCCTTCACTTCCAGCT 360
Db 13300 TCCACACTGCGGAGGAGCTGGGGACCCCGGACACCCGTCCTGCTGCCCTTCACTTCCAGCT 13359
Qy 361 CCGCCTCTCCGCGGAGACCCCGGCGCGCTCCGAGACCCCTCCGAGGTCCTCCGCGCGACGCC 420
Db 13360 CCGCCTCTCCGCGGAGACCCCGGCGCGCTCCGAGACCCCTCCGAGGTCCTCCGCGCGACGCC 13419
Qy 421 CCTCCGGGCGCTCCAGCGCTCCCTTCCCTTCCGCGGCGCGCGCTCCCTCTCCGCGCG 480
Db 13420 CCTCCGGGCGCTCCAGCGCTCCCTTCCCTTCCGCGGCGCGCGCTCCCTCTCCGCGCG 13479
Qy 481 CGAGTTTTCAGGACAGCGCTGCTGCTGCTGCGACAGTGGGAAGCCCTGCGCCCGGCGCACCC 540
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Db 13780 TCGCGGTCCGCTGGGTTGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13839
Qy 841 CAGCGACTCAGGGCGCTTCCCGCGCGAGTGTCTGCTGCTGAGGAGCTGGTGGCGCGAGT 900
Db 13840 CAGCGACTCAGGGCGCTTCCCGCGCGAGTGTCTGCTGCTGAGGAGCTGGTGGCGCGAGT 13899
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Qy 961 GCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1001
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US-10-023-969-1
; Sequence 1, Application US/10023969
; Publication No. US20030095989A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Irving, John
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Chimeric Cytolytic Viruses for Cancer Treatment
; FILE REFERENCE: 084,002
; CURRENT APPLICATION NUMBER: US/10/023,969
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/256,418
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-969-1

Query Match 100.0%; Score 1001; DB 5; Length 15418;
Best local Similarity 100.0%; Pred. No. 8.6e-206; Mismatches 0; Indels 0; Gaps 0;
Matches 1001; Conservative 0;

Qy 1 CGTCCGAGCCTGAGGAGCAGCCCTGGGTCTCGGATCAGGCGCAGCGCGCAAGGGTTCGCGC 60
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Qy 61 CAGCACTGTTCACAGGCTTCCACATCATATGAGCCCTTCCCTCGGGTTACCCCAAGCT 120
Db 13060 CAGCACTGTTCACAGGCTTCCACATCATATGAGCCCTTCCCTCGGGTTACCCCAAGCT 13119
Qy 121 AGGCCGATTGACCTCTCTCGCTGGGGCCCTGCTGCGCTGCTGCGCTGCTGCGCTGCGAGCGC 180
Db 13120 AGGCCGATTGACCTCTCTCGCTGGGGCCCTGCTGCGCTGCTGCGCTGCTGCGAGCGC 13179
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Db 13180 GAGCGCGCGCGCGCGGGAAGCGCGCCAGACCCCGGGTCCGCGCGCGAGCAGCTGCG 13239
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Qy 301 TCCACACTGCGGAGGAGCTGGGGACCCCGGCGCGCTGCGCGACCCGCTGCTGCGCGCTTCACTTCCAGCT 360
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Qy 661 TGCAGCGCGGAGACCCCGCGCGCTTTCGCGCGCTGCTGCGCGAGTGGCGCGCTGCGCGCG 720
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Qy 841 CAGCGACTCAGGGCGCTTCCCGCGCGAGTGTCTGCTGCTGAGGAGCTGGTGGCGCGAGT 900
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RESULT 9

US-10-811-012-1  
; Sequence 1, Application US/10811012  
; Publication No. US20040152189A1  
; GENERAL INFORMATION:  
; APPLICANT: Geron Corporation  
; APPLICANT: McWhir, Jim  
; APPLICANT: Gold, Joseph D.  
; APPLICANT: Schiff, J. Michael  
; TITLE OF INVENTION: Selective Antibody Targeting of Undifferentiated Stem Cells  
; FILE REFERENCE: 096,006D- SegList  
; CURRENT APPLICATION NUMBER: US/10/811,012  
; CURRENT FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER: 09/995,419  
; PRIOR FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 60/253,357  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/253,443  
; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/253,395  
; PRIOR FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 15418  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-811-012-1

Query Match 100.0%; Score 1001; DB 7; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 8.6e-206;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CGTCCGAGCTGAGGAGCGCGCTCGGCTCTCCGATCAGGCGCAGGCGCGCAAGAGGCTCGCGG 60  
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LOCATION: (21763)...(23851)  
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LOCATION: (23852)...(24032)  
OTHER INFORMATION: exon 4  
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LOCATION: (24720)...(24899)  
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NAME/KEY: exon  
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LOCATION: (30293)...(31272)  
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LOCATION: (31273)...(31358)  
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LOCATION: (37885)...(38073)  
OTHER INFORMATION: exon 11  
NAME/KEY: intron  
LOCATION: (38074)...(41874)  
OTHER INFORMATION: intron 11  
NAME/KEY: exon  
LOCATION: (41875)...(42001)  
OTHER INFORMATION: exon 12  
NAME/KEY: intron  
LOCATION: (42002)...(42881)  
OTHER INFORMATION: intron 12  
NAME/KEY: exon  
LOCATION: (42882)...(42943)  
OTHER INFORMATION: exon 13  
NAME/KEY: intron  
LOCATION: (42944)...(46129)  
OTHER INFORMATION: intron 13  
NAME/KEY: exon  
LOCATION: (46130)...(46254)  
OTHER INFORMATION: exon 14  
NAME/KEY: intron  
LOCATION: (46255)...(47035)  
OTHER INFORMATION: intron 14

NAME/KEY: exon  
LOCATION: (47036)...(47173)  
OTHER INFORMATION: exon 15  
NAME/KEY: intron  
LOCATION: (47174)...(47709)  
OTHER INFORMATION: intron 15  
NAME/KEY: exon  
LOCATION: (47710)...(50544)  
OTHER INFORMATION: exon 16  
US-09-733-294A-30  
Query Match 99.8%; Score 999.4; DB 3; Length 51552;  
Best Local Similarity 99.9%; Pred. No. 1.4e-205;  
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CGTCCGGACCTGGAGGAGCCCTGGGTCTCCGGATCAGGCGAGCGCCCAAGGGTTCGCGG 60  
Db 10729 CGTCCGGACCTGGAGGAGCCCTGGGTCTCCGGATCAGGCGAGCGCCCAAGGGTTCGCGG 10788  
Qy 61 CACGCACCTGTTCACAGGGCTCCACATCATATGCGCCCTCCCTCGGGTTTACCCACAGCCT 120  
Db 10789 CACGCACCTGTTCACAGGGCTCCACATCATATGCGCCCTCCCTCGGGTTTACCCACAGCCT 10848  
Qy 121 AGGCCGATTGACCTCTCTCGCTGGGCGCTCTCGTGGCGTCCCTGCAACCTTGGAGGCGC 180  
Db 10849 AGGCCGATTGACCTCTCTCGCTGGGCGCTCTCGTGGCGTCCCTGCAACCTTGGAGGCGC 10908  
Qy 181 GAGCGGCGCGGGGGGAGCGCGGCCACAGACCCCGGGTCCGCGGAGCAGCTGGC 240  
Db 10909 GAGCGGCGCGGGGGGAGCGCGGCCACAGACCCCGGGTCCGCGGAGCAGCTGGC 10968  
Qy 241 CTGTCCGGGCGAGGCCCGGGCTCCACATGAGTTTCGGGGCACAGACGCCACAGACCGCGCT 300  
Db 10969 CTGTCCGGGCGAGGCCCGGGCTCCACATGAGTTTCGGGGCACAGACGCCACAGACCGCGCT 11028  
Qy 301 TCCACGTTGCGGAGGAGCTGGGGACCGGGGACCCCGTCTTGGCCCTTTCACTTCCAGCT 360  
Db 11029 CCCCACGTGGCGAGGGACTGGGGACCCGGGACCCGCTCTCGCCCTTCACTTCCAGCT 11088  
Qy 361 CGGCTCTCTCGCGGGACCCCGCGCTCCGACCCCTCCCGGGTCCCGGGCCAGGCC 420  
Db 11089 CCGCTCTCTCGCGGGACCCCGCGCTCCGACCCCTCCCGGGTCCCGGGCCAGGCC 11148  
Qy 421 CCTCCGGGCTCTCCAGCCCTCCCTCTTCTTTCGGCGGCCCGCCCTCTCTCTCGCGGG 480  
Db 11149 CCTCGGGCTCTCCAGCCCTCCCTCTTCTTTCGGCGGCCCGCCCTCTCTCTCGCGGG 11208  
Qy 481 CGAGTTTCAGGACGCTGCTCTCTGTCGCAAGTGGGAAAGCCCTGGCCCGCGCACCC 540  
Db 11209 CGAGTTTCAGGACGCTGCTCTCTGTCGCAAGTGGGAAAGCCCTGGCCCGCGCACCC 11268  
Qy 541 CCGGATGCGCGGCTCTCCCGCTGCGAGCGCTGCGCTCTCTGTCGCGAGCCTACTACC 600  
Db 11269 CCGGATGCGCGGCTCTCCCGCTGCGAGCGCTGCGCTCTCTGTCGCGAGCCTACTACC 11328  
Qy 601 GCGAGTGTCTCGCTGCGCACGTTTCGTGCGCGCTGCGGGCCCGAGGGCTGGCGGCTGG 660  
Db 11329 GCGAGTGTCTCGCTGCGCACGTTTCGTGCGCGCTGCGGGCCCGAGGGCTGGCGGCTGG 11388  
Qy 661 TGCAGCGCGGGACCCCGCGCTTTCGCGCGCTGCTGTCGCGCCAGTCTCTGTCGTCGTC 720  
Db 11389 TGCAGCGCGGGACCCCGCGCTTTCGCGCGCTGCTGTCGCGCCAGTCTCTGTCGTCGTC 11448  
Qy 721 CCGGAGCGACGCGCGCGCTCCCGCTGCGAGCGCTGCGCTCTCTGCGCCAGTGGGCTCCCCGGG 780  
Db 11449 CCGGAGCGACGCGCGCGCTCCCGCTGCGAGCGCTGCGCTCTCTGCGCCAGTGGGCTCCCCGGG 11508  
Qy 781 TCGCGTCCGCTGGGTTGAGGGCGCGCGGGGACACAGCAGCATCGAGAGCAGCG 840  
Db 11509 TCGCGTCCGCTGGGTTGAGGGCGCGCGGGGACACAGCAGCATCGAGAGCAGCG 11568  
Qy 841 CAGCGACTCAGGGCGCTTCCCGCGAGTGTCTGCTGAGGAGCTGGTGGCCCGAGT 900







QY 477 GCGCGAGTTTCAGGACGCTGCGTCTGCTGCGACAGTGGAGCCCTGCGCCCGGCC 536  
Db 2427 GCGCGAGTTTCAGGACGCTGCGTCTGCTGCGACAGTGGAGCCCTGCGCCCGGCC 2486  
QY 537 ACCCCCGGATGCGCGCGCTCCCGCTGCGAGCCGTCGCTGCTGCGAGCCAC 596  
Db 2487 ACCCCCGGATGCGCGCGCTCCCGCTGCGAGCCGTCGCTGCTGCGAGCCAC 2546  
QY 597 TACCGGAGTGTGCGCGCTGCGACGTTCTGCGCGCCCTGGGSCCCAGCGCTGGCGG 656  
Db 2547 TACCGGAGTGTGCGCGCTGCGACGTTCTGCGCGCCCTGGGSCCCAGCGCTGGCGG 2606  
QY 657 CTGTGTCAGCGCGGACCCCGCGCTTTTCGCGCGCTGCTGCGCCAGTGTGTC 716  
Db 2607 CTGTGTCAGCGCGGACCCCGCGCTTTTCGCGCGCTGCTGCGCCAGTGTGTC 2666  
QY 717 GTGCCCTGGAGCAGCGCGCCCGCGCGCCCTCTCTTCGCGCAGGTGGCCCTCC 776  
Db 2667 GTGCCCTGGAGCAGCGCGCCCGCGCGCCCTCTCTTCGCGCAGGTGGCCCTCC 2726  
QY 777 GGGGTGCGGCTCCGCTGCGGCTGAGGCGCGCGCGGCGGAGACGACATGCGGAGC 836  
Db 2727 GGGGTGCGGCTCCGCTGCGGCTGAGGCGCGCGCGGCGGAGACGACATGCGGAGC 2786  
QY 837 AGCGCAGGCGACTCAGGCGCTTCCCGCGCAGGTGTCTGCTGAGGAGCTGTGGGCC 896  
Db 2787 AGCGCAGGCGACTCAGGCGCTTCCCGCGCAGGTGTCTGCTGAGGAGCTGTGGGCC 2846  
QY 897 GAGTCTGCGAGGCTGTGCGAGCGCGCGCGAGAACGTCGTGCGCTTGGCTTGGCGC 956  
Db 2847 GAGTCTGCGAGGCTGTGCGAGCGCGCGCGAGAACGTCGTGCGCTTGGCTTGGCGC 2906  
QY 957 TGCTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1001  
Db 2907 TGCTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2951

RESULT 15

US-10-044-692-6  
; Sequence 6, Application US/10044692  
; Publication No: US20030096344A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
; THERAPEUTIC METHODS  
; NUMBER OF SEQUENCES: 335  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/044,692  
; FILING DATE: 11-Jan-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/912,951  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002600US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4200 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-044-692-6  
Query Match 92.6%; Score 926.8; DB 5; Length 4200;  
Best Local Similarity 98.3%; Pred. No. 9.5e-190;  
Matches 989; Conservative 0; Mismatches 12; Indels 5; Gaps 5;  
QY 1 CGTCCGACCTGAGGAGCGCCCTGGGTCTCCGATTCAGGCGAGCGGCCAAGAGGTGCGCG 60  
Db 1763 CGTCCGACCTGAGGAGCGCCCTGGGTCTCCGATTCAGGCGAGCGGCCAAGAGGTGCGCG 1822  
QY 61 CACGACCTGTTCAGGCGCTCCACATCATGCGCCCTCCCTCGGTTACCCACAGCCT 120  
Db 1823 CACGACCTGTTCAGGCGCTCCACATCATGCGCCCTCCCTCGGTTACCCACAGCCT 1882  
QY 121 AGGCC-GATTTCGACTCTCTCGCTGGGGCCCTCG-CTGGCGTCTCCTGCACCTCGGAGC 178  
Db 1883 AGGCCGATTTCGACTCTCTCTCGCTGGGGCCCTCGCTGGCGTCTCCTGCACCTCGGAGC 1942  
QY 179 GCGAGCGCGCGCGCGGGGGAAGCGCGGCCAGACCCCGGGTCCGCCCGG-AGCAGCT 237  
Db 1943 GCGAGCGCGCGCGCGGGGGAAGCGCGGCCACATACCCCGGGTCCGCCCGGAGCAGCT 2002  
QY 238 GCGCTGTGCGGGCGAGCGCGGGCTCCAGTGTGATTCGCGGGGACAGAGCGCCAGACCGC 297  
Db 2003 GCGCTGTGCGGGCGAGCGCGGGCTCCAGTGTGATTCGCGGGGACAGAGCGCCAGACCGC 2062  
QY 298 GCTTCCACGTCGCGGAGGAGCTGGGACCCGCGGACCCGCTCTCGCCCTTTCACCTTCCA 357  
Db 2063 GCTTCCACGTCGCGGAGGAGCTGGGACCCGCGGACCCGCTCTCGCCCTTTCACCTTCCA 2122  
QY 358 GCTCGGCTCTCTCGCGCGGACCCCGCGCCCTTCGCGACCCCTTCGCGGGTCCCGGCCAG 417  
Db 2123 GCTCGGCTCTCTCGCGCGGACCCCGCGCCCTTCGCGAACCCCTTCGCGGTCGCGGCCAG 2182  
QY 418 CCCCCTCGGGGCTTCCAGCGCCCTCCCTCTCC-TTTTCGGGGCGCCGCGCTCTCC-TCG 475  
Db 2183 CCCCCTCGGGGCTTCCAGCGCCCTCCCTCTCCCTTTTCGCGGGCGCCGCGCTCTCTTCG 2242  
QY 476 CGGCGCAGGTTTCAGGCGAGCGCTGCTGTCGCGCAGTGGGAGCCCTGCGCCCGCGC 535  
Db 2243 CGGCGCAGGTTTCAGGCGAGCGCTGCTGTCGCGCAGTGGGAGCCCTGCGCCCGCGC 2302  
QY 536 CACCCCGCGATGCGCGCGCTCCCGCTGCGGAGCCGTCGCTCCCTGTCGCGAGCCA 595  
Db 2303 CACCCCGCGATGCGCGCGCTCCCGCTGCGGAGCCGTCGCTCCCTGTCGCGAGCCA 2362  
QY 596 CTACCGCAGGTGTCGCGCTGGCCACAGTTGTCGGGGCGCTTGGGGGCGCCAGGGTGGCG 655  
Db 2363 CTACCGCAGGTGTCGCGCTGGCCACAGTTGTCGGGGCGCTTGGGGGCGCCAGGGTGGCG 2422

Qy	656	GCTGGTGACGCGCGGACCCGCGGCTTTCCGCGCTGTGTGCCAGTGCCCTGGTGTG	715
Db	2423	GCTGGTGACGCGCGGACCCGCGGCTTTCCGCGCTGTGTGCCAGTGCCCTGGTGTG	2482
Qy	716	CGTGCCCTGGGAACGCAAGCGCGCCCCCGCGCCCCCTCTTCCGCAAGGTGGCCCTCCC	775
Db	2483	CGTGCCCTGGGAACGCAAGCGCGCCCCCGCGCCCCCTCTTCCGCAAGGTGGCCCTCCC	2542
Qy	776	CGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGAACGAGCGACATGCGGAGAG	835
Db	2543	CGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGAACGAGCGACATGCGGAGAG	2602
Qy	836	CAGCGCAGGCGACTCAGGGCGCTTCCCGCCGCGAGGTGTCTGCTGAAGGAGCTGGTGCC	895
Db	2603	CAGCGCAGGCGACTCAGGGCGCTTCCCGCCGCGAGGTGTCTGCTGAAGGAGCTGGTGCC	2662
Qy	896	CGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGTGGCTTTCGGCTTCGCG	955
Db	2663	CGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGTGGCTTTCGGCTTCGCG	2722
Qy	956	CTGCTGACCGGGGCCCGGGGGCCCCCGAGGCCCTTCACCA	1001
Db	2723	CTGCTGACCGGGGCCCGGGGGCCCCCGAGGCCCTTCACCA	2768

Search completed: January 10, 2006, 20:35:13  
Job time : 951.333 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 05:46:59 ; Search time 690.667 Seconds  
(without alignments)  
9659.301 Million cell updates/sec

Title: US-09-615-039-1\_COPY\_13000\_14000  
Perfect score: 1001  
Sequence: 1 cgtccgacctggaggcgc.....ccccgagccttcaccacca 1001

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq 21.\*

- 1: geneseqn1980s.\*
- 2: geneseqn1990s.\*
- 3: geneseqn2000s.\*
- 4: geneseqn2001as.\*
- 5: geneseqn2001bs.\*
- 6: geneseqn2002as.\*
- 7: geneseqn2002bs.\*
- 8: geneseqn2003as.\*
- 9: geneseqn2003bs.\*
- 10: geneseqn2003cs.\*
- 11: geneseqn2003ds.\*
- 12: geneseqn2004as.\*
- 13: geneseqn2004bs.\*
- 14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	1001	100.0	2501	14 ADV97952	Adv97952 Human tum
C 2	1001	100.0	7928	14 AEA18025	Aea18025 Human gyn
C 3	1001	100.0	15418	3 AAE63785	Aae63785 Nucleotid
C 4	1001	100.0	15418	6 AAL38601	Aal38601 Human TER
C 5	1001	100.0	15418	6 ABS54997	Abs54997 Lambda cl
C 6	1001	100.0	15418	6 AAL38595	Aal38595 DNA of pl
C 7	1001	100.0	15418	10 ADC21253	Adc21253 Lambda cl
C 8	999.4	99.8	5491	13 ADU82631	Adu82631 Human hTE
C 9	999.4	99.8	51552	6 AAS96607	Aas96607 DNA encod
C 10	945.8	94.5	4335	2 AAV16979	Aav16979 Human tel
C 11	905	90.4	4356	13 ADU82633	Adu82633 Human hTE
C 12	867.6	86.7	4293	14 ADV23865	Adv23865 Human hTE
C 13	866.4	86.6	2043	14 ADV23882	Adv23882 Human hTE
C 14	629.8	62.9	2501	14 ADV98042	Adv98042 Bisulfite
C 15	629.8	62.9	7928	14 AEA18046	Aea18046 Converted
C 16	582	58.1	3962	4 AAH41091	Aah41091 Telomeras
C 17	572.2	57.2	4356	6 ABL92335	Ab192335 Chemical
C 18	546.4	54.6	5126	2 AAX88272	Aax88272 Human cat
C 19	521.4	52.1	2501	14 ADV98043	Adv98043 Bisulfite

C 20	521.4	52.1	7928	14 AEA18047	Aea18047 Converted
C 21	502.2	50.2	35871	6 AAD27972	Aad27972 Recombina
C 22	502.2	50.2	35978	6 AAD27971	Aad27971 Recombina
C 23	499	49.9	1677	6 AAD27973	Aad27973 Human tel
C 24	460.8	46.0	4356	6 ABL92334	Ab192334 Chemical
C 25	456	45.6	3500	2 AAX18275	Axi18275 Telomeras
C 26	455	45.5	3543	8 ABZ69628	Abz69628 Plasmid c
C 27	453.4	45.3	455	12 ADI33422	Adi33422 Human tel
C 28	442.6	44.2	2501	14 ADV98136	Adv98136 Bisulfite
C 29	442.6	44.2	7928	14 AEA18066	Aea18066 Converted
C 30	412.4	41.2	496	13 ADT77582	Adt77582 hTERT min
C 31	412.4	41.2	8565	13 ADT77585	Adt77585 TSTA-hTER
C 32	411	41.1	902	13 ADR73427	Adr73427 Human m-h
C 33	408	40.8	408	13 ADR73423	Adr73423 Human tel
C 34	397	39.7	397	6 ABS98658	Abs98658 Human TER
C 35	397	39.7	397	14 ADZ08730	Adz08730 Human TER
C 36	390.4	39.0	460	14 ADV23870	Adv23870 Human hTE
C 37	389.6	38.9	454	11 ADN00285	Adn00285 Tumour-sp
C 38	376.4	37.6	378	8 ACC47272	Acc47272 CEA gene
C 39	334.8	33.4	2501	14 ADV98137	Adv98137 Bisulfite
C 40	334.8	33.4	7928	14 AEA18067	Aea18067 Converted
C 41	329.6	32.9	1404	6 AAD22344	Aad22344 Chemical
C 42	324	32.4	324	13 ADW76702	Adw76702 DNA relat
C 43	300	30.0	3972	2 AAV72125	Aav72125 Human cat
C 44	300	30.0	4042	2 AAV72117	Aav72117 Human cat
C 45	298.2	29.8	314	3 AAA94134	Aaa94134 Telomeras

ALIGNMENTS

RESULT 1

ADV97952/c  
ID ADV97952 standard; DNA; 2501 BP.

XX AC ADV97952;

XX 10-MAR-2005 (first entry)

DE Human tumor-associated cancer-testis antigen tert DNA Seq 44.

XX ds; immunotherapy; DNA methylation; tumor-associated antigen; cancer;  
XX cytostatic; vaccine; text.

XX OS Homo sapiens.

XX PN EPI491639-A2.

XX PD 29-DEC-2004.

XX PF 17-JUN-2004; 2004EP-00090238.

XX PR 24-JUN-2003; 2003DE-01029240.

XX (EPIG-) EPIGENOMICS AG.

XX Eichler-Mertens M, Piepenbrock C, Olek A;

XX WPI; 2005-050366/06.

PT Identifying target points for immunotherapy of tumors by analysis of  
PT methylation status of many tumor-associated antigens, also treatment,  
PT particularly vaccination, using selected antigens.

XX Disclosure; SEQ ID NO 44; 206pp; German.

XX This invention relates to a novel method for determining target points  
XX for tumor immunotherapy by taking a DNA sample from serum or other bodily  
XX fluids of a patient. Specifically, it refers to identifying the  
XX methylation status of at least one CpG island in each of 47 identified  
XX tumor-associated antigens in order to generate a methylation pattern from  
XX the results. It describes an analysis of methylation status that includes  
XX chemical treatment of DNA with a bisulfite, optionally followed by

CC amplification, particularly methylation specific PCR (MSP) and/ or a  
CC heavy methyl technique. Accordingly, the present invention provides tumor  
CC associated antigen sequences and also the corresponding bisulfite  
CC sequences generated under differing methylation conditions. As such, the  
CC method can be used to identify targets for immunotherapy of cancers,  
CC specifically by vaccination against selected tumor-associated antigens to  
CC provide individualized immunotherapy. Furthermore, the method allows  
CC simultaneous determination of methylation status of many tumor antigens  
CC and also of other methylation-regulated cofactors important for  
CC vaccination. The pharmaceutical compositions derived thereof exhibit  
CC cytostatic activity and can be used in the development of vaccines. This  
CC polynucleotide sequence is a human tumor associated cancer-testis antigen  
CC DNA sequence of the invention.  
XX  
SQ Sequence 2501 BP; 504 A; 767 C; 827 G; 403 T; 0 U; 0 Other;

Query Match 100.0%; Score 1001; DB 14; Length 2501;  
Best Local Similarity 100.0%; Pred. No. 8.1e-138;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCAGCGGCAAAAGGTCCCG 60  
DB 1046 CGTCCGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCAGCGGCAAAAGGTCCCG 987  
QY 61 CACGACCTGTCCAGGCTCCACATCATATGCGCCCTCCCTGGGTACCCACAGCCT 120  
DB 986 CACGACCTGTCCAGGCTCCACATCATATGCGCCCTCCCTGGGTACCCACAGCCT 927  
QY 121 AGCCCGATTGACCTCTCTCGTGGGGCCCTCGCTGGCGTCCCTGACCCCTGGAGCGC 180  
DB 926 AGCCCGATTGACCTCTCTCGTGGGGCCCTCGCTGGCGTCCCTGACCCCTGGAGCGC 867  
QY 181 GAGCGGCGCGGGGAGAGCGGCGCCAGACCCCGGGTCCCGGAGCAGCTGCG 240  
DB 866 GAGCGGCGCGGGGAGAGCGGCGCCAGACCCCGGGTCCCGGAGCAGCTGCG 807  
QY 241 CTGTCCGGGCGAGCGCGGCTCCAGTGGATTGCGGGGACAGAGCCAGAGCCGCGCT 300  
DB 806 CTGTCCGGGCGAGCGCGGCTCCAGTGGATTGCGGGGACAGAGCCAGAGCCGCGCT 747  
QY 301 TCCACAGTGGCGAGGACCTGGGACCCGGGACCCCGTCTCGCCCTTACCTTCCAGCT 360  
DB 746 TCCACAGTGGCGAGGACCTGGGACCCGGGACCCCGTCTCGCCCTTACCTTCCAGCT 687  
QY 361 CCGCTCTCTCGCGAGACCCCGCTCGTCCGACCCCTCCCGGTCCCGGCGCAGCC 420  
DB 686 CCGCTCTCTCGCGAGACCCCGCTCGTCCGACCCCTCCCGGTCCCGGCGCAGCC 627  
QY 421 CTTCCGGGCTCCAGCCCTCCCTTCTTTCCGGGCGCCCGCTCTCTCGGGCG 480  
DB 626 CTTCCGGGCTCCAGCCCTCCCTTCTTTCCGGGCGCCCGCTCTCTCGGGCG 567  
QY 481 CGAGTTTCAGGACGCTGGTCTCTGTGGCGACGCTGGGAGCCCTGGCCCGCCACCC 540  
DB 566 CGAGTTTCAGGACGCTGGTCTCTGTGGCGACGCTGGGAGCCCTGGCCCGCCACCC 507  
QY 541 CCGGATGCGCGGCTCCCGCTGCGAGCGGTGCTCTCTGCTGCGAGCAGCTACC 600  
DB 506 CCGGATGCGCGGCTCCCGCTGCGAGCGGTGCTCTCTGCTGCGAGCAGCTACC 447  
QY 601 GCAGGTGCTGCGCTGGCCAGCTTGTGGCGGCTGGGGCCCGAGGCTGGGGGTGG 660  
DB 446 GCAGGTGCTGCGCTGGCCAGCTTGTGGCGGCTGGGGCCCGAGGCTGGGGGTGG 387  
QY 661 TGACGCGCGGGGACCCCGGCTTTCGCGCGCTGTGGGCCAGTGTGCTGTGCTGC 720  
DB 386 TGACGCGCGGGGACCCCGGCTTTCGCGCGCTGTGGGCCAGTGTGCTGTGCTGC 327  
QY 721 CTTGGGACGACGCGCGCCCGCCCGCTCTCTTCGCGCAGGTGGCTCCCGGGG 780  
DB 326 CTTGGGACGACGCGCGCCCGCCCGCTCTCTTCGCGCAGGTGGCTCCCGGGG 267  
QY 781 TCGCGCTCGGCTGGGTGTAGGGGCGCGCGGGGGAACAGGCATGCGGAGCAGCG 840

DB 266 TCGCGTCCGGCTGGGTTGAGGGCGCGCGGGGGAACGACGACATGCGGAGAGCAGCG 207  
QY 841 CAGCGGACTCAGGGCGCTTCCCGCGCAGGTGCTCTGCTGAAGAGTGTGTGGCCGAGT 900  
DB 206 CAGCGGACTCAGGGCGCTTCCCGCGCAGGTGCTCTGCTGAAGAGTGTGTGGCCGAGT 147  
QY 901 GCTGCGAGGCTCTGCGAGCGCGCGCGGAGACGTCGCTTGGCTTGGGCTTGGGCTGCT 960  
DB 146 GCTGCGAGGCTGTGCGAGCGCGCGCGGAGACGTCGCTTGGCTTGGGCTTGGGCTGCT 87  
QY 961 GGAAGCGGCGCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1001  
DB 86 GGAAGCGGCGCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 46

RESULT 2

ARE18025/c  
ID ARE18025 standard; DNA; 7928 BP.

XX ARE18025;  
XX AC  
XX DT 11-AUG-2005 (first entry)  
XX Human gynecological cell proliferative disorder gene SEQ ID NO 11.  
XX detection; prognosis; cell proliferative disorder; cervical cancer;  
XX endometrial cancer; neoplasia; cancer; ds.  
XX Homo sapiens.  
XX WO2005049861-A2.  
XX 02-JUN-2005.  
XX 10-NOV-2004; 2004WO-EP012740.  
XX 10-NOV-2003; 2003EP-00025739.  
XX (EPIG-) EPIGENOMICS AG.  
XX Widschwendter M;  
XX WFI; 2005-396129/40.  
XX Detecting, differentiating, and prognosing a gynecological cell  
XX proliferative disorder by obtaining a cervicovaginal secretion specimen  
XX from an individual and determining the methylation status of at least one  
XX or more CpG positions.  
XX Claim 3; SEQ ID NO 11; 163pp; English.

XX The invention relates to a method of detecting, differentiating, and  
XX prognosing a gynecological cell proliferative disorder comprising  
XX obtaining a cervicovaginal secretion specimen from an individual,  
XX determining the methylation status of at least one or more CpG positions,  
XX and/or prognosing a gynecological cell proliferative disorder in the  
XX individual. The method is useful for detecting, differentiating, and  
XX prognosing a gynecological cell proliferative disorder, e.g. dysplasia or  
XX low-grade squamous intraepithelial lesions, high-grade squamous  
XX intraepithelial lesions, cervical cancer, endometrial cancer, or grade 1  
XX to 3 cervical intraepithelial neoplasia. The present sequence represents  
XX a human gynecological cell proliferative disorder related gene.

SQ Sequence 7928 BP; 1629 A; 2721 C; 2411 G; 1167 T; 0 U; 0 Other;

Query Match 100.0%; Score 1001; DB 14; Length 7928;  
Best Local Similarity 100.0%; Pred. No. 6.7e-138;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCAGCGGCAAAAGGTCCCG 60  
|||



Db 6473 GTCGCGACCTGGAGGACGACCTCGGCTCTCGGATCAGGCCAGCGGCCAAAGGGTCGCGC 6414  
QY 61 CACGACCTGTTCCAGGGCTCCACATCATGGCCCTCCCTCGGGTTACCCACAGCCT 120  
Db 6413 CACGACCTGTTCCAGGGCTCCACATCATGGCCCTCCCTCGGGTTACCCACAGCCT 6354  
QY 121 AGGCGATTGCACTCTCTCCGCTGGGCGCTCGCTGCGTCCCTGCACTCCCTGGAGCGC 180  
Db 6353 AGGCGATTGCACTCTCTCCGCTGGGCGCTCGCTGCGTCCCTGCACTCCCTGGAGCGC 6294  
QY 181 GAGCGCGCGCGGGGAGCGCGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTCGC 240  
Db 6293 GAGCGCGCGCGGGGAGCGCGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTCGC 6234  
QY 241 CTGTCGGGGCAGCGCGCGCTCCAGTGAATTCGGGGACAGACGCGCCAGCGACCGGCT 300  
Db 6233 CTGTCGGGGCAGCGCGCGCTCCAGTGAATTCGGGGACAGACGCGCCAGCGACCGGCT 6174  
QY 301 TCCCACTGGCGGAGGACTGGGACCCCGGGACCCGCTCTGCGCCCTTCACTTCCAGCT 360  
Db 6173 TCCCACTGGCGGAGGACTGGGACCCCGGGACCCGCTCTGCGCCCTTCACTTCCAGCT 6114  
QY 361 CGGCTCTCGCGCGGACCCCGCGCCCTCGGACCCCTCGGGTCCGCCCGGAGCGC 420  
Db 6113 CGGCTCTCGCGCGGACCCCGCGCCCTCGGACCCCTCGGGTCCGCCCGGAGCGC 6054  
QY 421 CCTCGGGCCCTCCAGCGCCCTCCCTTCTTTCGGGGCCCGGCTCTCTCGCGCG 480  
Db 6053 CCTCGGGCCCTCCAGCGCCCTCCCTTCTTTCGGGGCCCGGCTCTCTCGCGCG 5994  
QY 481 CGAGTTTCAGGACGCGCTCGCTGCTGCGACGTTGGGAAAGCCCTGCGCCCGGACCC 540  
Db 5993 CGAGTTTCAGGACGCGCTCGCTGCTGCGACGTTGGGAAAGCCCTGCGCCCGGACCC 5934  
QY 541 CCGGATCGCGCGCTCCGCTCGCGAGCGCTCGCTCTCTGTCGGGAGCCTACCTACC 600  
Db 5933 CCGGATCGCGCGCTCCGCTCGCGAGCGCTCGCTCTCTGTCGGGAGCCTACCTACC 5874  
QY 601 GCGAGTCTCGCTGCGTCCAGTTCGTCGCGCGCTCGCGCGCCCGGAGGTCGGGCTGG 660  
Db 5873 GCGAGTCTCGCTGCGTCCAGTTCGTCGCGCGCTCGCGCGCCCGGAGGTCGGGCTGG 5814  
QY 661 TCGAGCGGGGACCCCGCGCTTTCGCGCGCTGCTGCGCGCTGCTGCTGCTGCTGCTG 720  
Db 5813 TCGAGCGGGGACCCCGCGCTTTCGCGCGCTGCTGCGCGCTGCTGCTGCTGCTGCTG 5754  
QY 721 CTTGGGACGACGCGCGCGCGCGCTCTCTTTCGCGAGGTCGGCTTCCCGCGGG 780  
Db 5753 CTTGGGACGACGCGCGCGCGCGCTCTCTTTCGCGAGGTCGGCTTCCCGCGGG 5694  
QY 781 TCGCGCTCGGCTGGGTTGAGGGCGCGCGGGGAAACGAGCATGCGGAGCAGCG 840  
Db 5693 TCGCGCTCGGCTGGGTTGAGGGCGCGCGGGGAAACGAGCATGCGGAGCAGCG 5634  
QY 841 CAGGCGACTCAGGGCGCTTCCCGCGAGTGTCTGCTGCTGAGGAGCTGGTGGCCCGAGT 900  
Db 5633 CAGGCGACTCAGGGCGCTTCCCGCGAGTGTCTGCTGCTGAGGAGCTGGTGGCCCGAGT 5574  
QY 901 GCTGAGAGGCTGTGCGAGCGCGCGGAGAAAGCTGTGCGCTTTCGCGCTGCTGCTGCT 960  
Db 5573 GCTGAGAGGCTGTGCGAGCGCGCGGAGAAAGCTGTGCGCTTTCGCGCTGCTGCTGCT 5514  
QY 961 GGAGGGGCGCGCGGGGCGCGCGCGCTTTCACACCA 1001  
Db 5513 GGAGGGGCGCGCGGGGCGCGCGCGCTTTCACACCA 5473

RESULT 3  
AAA63785  
ID AAA63785 standard; DNA; 15418 BP.  
XX AC  
XX AAA63785;

DT 04-DEC-2000 (first entry)  
XX Nucleotide sequence of the human TERT promoter and gene from pGRN142.  
DE Telomerase reverse transcriptase; TERT; promoter; telomerase complex;  
XX telomere length; hyperplastic disease; cancer; oncolytic virus;  
KW cis-acting transcriptional control sequence; viral replication;  
KW cell proliferation; aging; immunological disorder; infertility; ss.  
XX Homo sapiens.  
XX WO200046355-A2.  
PN 10-AUG-2000.  
PD 04-FEB-2000; 2000WO-US003104.  
PF 04-FEB-1999; 99US-00244438.  
PR (GERO-) GERON CORP.  
XX Morin GB, Lichtsteiner S, Vasserot A, Adams R, Cardoza LM;  
PI Lebkowski JS;  
XX WPI; 2000-532898/48.  
XX New polynucleotides comprising cis-acting transcriptional control  
PT sequences, e.g. promoter sequence, of telomerase reverse transcriptase  
PT genes, useful in the treatment of cancer.  
XX Claim 9; Page 58-61; 63pp; English.  
XX The present sequence represents the human telomerase reverse  
CC transcriptase (TERT) promoter and gene. TERT is part of the telomerase  
CC complex responsible for maintaining telomere length and increasing  
CC replicative capacity of progenitor cells. Telomerase activity is turned  
CC off in mature differentiated cells, but is turned back on again in  
CC hyperplastic diseases, including many cancers. The polynucleotide  
CC comprises cis-acting transcriptional control sequences, e.g. promoter  
CC sequences. These promoter sequences are used to produce oncolytic viruses,  
CC in which a toxin or genetic element essential for viral replication is  
CC placed under the control of a TERT promoter. As a result, the virus  
CC replicates preferentially in cells expressing TERT, and selectively lyses  
CC cancer cells. The oncolytic viruses are useful for treating cancer in  
CC humans or animals. The TERT promoter sequences are useful in the  
CC treatment of cancer and other diseases of cell proliferation such as  
CC degenerative and aging processes and diseases of aging, immunological  
CC disorders, or infertility  
SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1001; DB 3; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 6e-138;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTCGCGACCTGGAGGACGACCTCGGCTCTCGGATCAGGCCAGCGGCCAAAGGGTCGCGC 60  
Db 13000 CGTCGCGACCTGGAGGACGACCTCGGCTCTCGGATCAGGCCAGCGGCCAAAGGGTCGCGC 13059  
QY 61 CACGACCTGTTCCAGGGCTCCACATCATGGCCCTCCCTCGGGTTACCCACAGCCT 120  
Db 13060 CACGACCTGTTCCAGGGCTCCACATCATGGCCCTCCCTCGGGTTACCCACAGCCT 13119  
QY 121 AGGCGATTGCACTCTCTCGCTGGGCGCTCGCTGCGTCCCTGCACTCCCTGGAGCGC 180  
Db 13120 AGGCGATTGCACTCTCTCGCTGGGCGCTCGCTGCGTCCCTGCACTCCCTGGAGCGC 13179  
QY 181 GAGCGCGCGCGGGGAGCGCGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTCGC 240  
Db 13180 GAGCGCGCGCGGGGAGCGCGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTCGC 13239  
QY 241 CTGTCGGGGCAGCGCGCGCTCCAGTGAATTCGGGGACAGACGCGCCAGCGACCGGCT 300

Db 13240 CTGTCGGGGCAGGCGCGGCTCCAGTGGATTGCGGGGCACAGAGCGCCAGAGCGCGCT 13299  
Qy 301 TCCACAGTGGCGGAGGAGACTGGGGACCCGGGACACCGCTCTGTCGCCCTTCACTTCCAGCT 360  
Db 13300 TCCACAGTGGCGGAGGAGACTGGGGACCCGGGACACCGCTCTGTCGCCCTTCACTTCCAGCT 13359  
Qy 361 CCGCTCTCTCGGCGGAGACCCCGGCGCTCCGACCCCTCCGGGTCCCGGGCCCGGCGCACGCC 420  
Db 13360 CCGCTCTCTCGGCGGAGACCCCGGCGCTCCGACCCCTCCGGGTCCCGGGCCCGGCGCACGCC 13419  
Qy 421 CTTCCGGGCGCTCCAGCGCTCCCTCTCTCTTTCGGCGGCGCCCGCCCTCTCTCTCGCGGCG 480  
Db 13420 CTTCCGGGCGCTCCAGCGCTCCCTCTCTCTTTCGGCGGCGCCCGCCCTCTCTCTCGCGGCG 13479  
Qy 481 CGAGTTTCAGGACGCTGCTGCTGCGACAGTGGGAAGCCCTGGCCCGGCGCACCC 540  
Db 13480 CGAGTTTCAGGACGCTGCTGCTGCGACAGTGGGAAGCCCTGGCCCGGCGCACCC 13539  
Qy 541 CCGGATGCGCGGCTCCCGGCTGCGAGCGCTGCGCTCTCTGCTGCGGAGCACTACC 600  
Db 13540 CCGGATGCGCGGCTCCCGGCTGCGAGCGCTGCGCTCTCTGCTGCGGAGCACTACC 13599  
Qy 601 GCGAGGTGCTGCGCTGCGCACAGTTCTGTCGGGCGCTTGGGCGCCCGAGGCTGGCGGTGG 660  
Db 13600 GCGAGGTGCTGCGCTGCGCACAGTTCTGTCGGGCGCTTGGGCGCCCGAGGCTGGCGGTGG 13659  
Qy 661 TGCAGCGCGGGACCCGGCGGCTTTTCGCGCGCTGCTGTCGCGCCAGTGCCTGCTGTGCGTGC 720  
Db 13660 TGCAGCGCGGGACCCGGCGGCTTTTCGCGCGCTGCTGTCGCGCCAGTGCCTGCTGTGCGTGC 13719  
Qy 721 CCTGGGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780  
Db 13720 CCTGGGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13779  
Qy 781 TCGCGCTGCGGCTGGGGTTGAGGCGGCGCGGGGGAACAGCGACATGCGGAGAGCAGCG 840  
Db 13780 TCGCGCTGCGGCTGGGGTTGAGGCGGCGCGGGGGAACAGCGACATGCGGAGAGCAGCG 13839  
Qy 841 CAGCGACTCAGGCGCTTCCCGCGCAGGTGTCTGCTGAAGGAGCTGGTGGGCCCGAGT 900  
Db 13840 CAGCGACTCAGGCGCTTCCCGCGCAGGTGTCTGCTGAAGGAGCTGGTGGGCCCGAGT 13899  
Qy 901 GCTGCGAGGCTGTGCGAGCGCGCGCGGCGGAAGAGCTGCTGGCCTTCCGGCTTCCGGCTGCT 960  
Db 13900 GCTGCGAGGCTGTGCGAGCGCGCGCGGCGGAAGAGCTGCTGGCCTTCCGGCTTCCGGCTGCT 13959  
Qy 961 GGAAGCGGCGCGCGGGGCGCGCGCGGCGGCTTCCAGCACCA 1001  
Db 13960 GGAAGCGGCGCGCGGGGCGCGCGCGGCGGCTTCCAGCACCA 14000

RESULT 4

AA138601  
ID AA138601 standard; DNA; 15418 BP.  
XX AC AA138601;  
XX AC  
XX AC  
DT 16-AUG-2002 (first entry)  
XX DE Human TERT promoter and upstream sequence.  
XX KW Cytostatic; glycosyltransferase; tumour; cell-surface carbohydrate;  
XX KW tissue specific; transcriptional control element; cancer cell;  
XX KW gene therapy; human TERT; telomerase reverse transcriptase; ds.  
XX OS Homo sapiens.  
XX PN WO200242468-A2.  
XX PD 30-MAY-2002.  
XX PF 26-NOV-2001; 2001WO-US044306.  
XX

PR 27-NOV-2000; 2000US-0253395P.  
XX (GERO-) GERON CORP.  
XX PI Schiffr MJ;  
XX WPI; 2002-479954/51.  
XX PT New polynucleotide encoding glycosyltransferase enzymes including histo  
PT blood group transferase useful for treating conditions associated with  
PT hyperproliferation, such as cancers and other neoplasias.  
XX PS Claim 9; Page 17-20; 49pp; English.  
XX CC The invention relates to a polynucleotide comprising an encoding sequence  
CC for a glycosyltransferase, under control of a heterologous tumour  
CC specific or tissue specific transcriptional control element, where  
CC expression of the polynucleotide in a human cell causes the cell to  
CC express a cell-surface carbohydrate determinant to which some or all  
CC humans have a naturally occurring antibody. The polynucleotide of the  
CC invention is useful for killing cancer cells and for preparing a  
CC medication for the treatment of cancer. The polynucleotide sequence of  
CC the invention can be used to treat disorders by gene therapy. This  
CC polynucleotide sequence represents the human TERT (telomerase reverse  
CC transcriptase) promoter and upstream sequence related to the invention  
XX SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1001; DB 6; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 6e-138;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CGTCCGACCTGAGGAGCGCCCTGGGCTTCGGATCAGGCGAGCGGCAAGGCTGCGCG 60  
Db 13000 CGTCCGACCTGAGGAGCGCCCTGGGCTTCGGATCAGGCGAGCGGCAAGGCTGCGCG 13059  
Qy 61 CAGCGACCTGTTCCAGGGCTCCATCATATGCGCCCTCCCTGGGTACCCACAGCCT 120  
Db 13060 CAGCGACCTGTTCCAGGGCTCCATCATATGCGCCCTCCCTGGGTACCCACAGCCT 13119  
Qy 121 AGCGCATTCAGCTCTCTCCGCTGGGGCTCGCTGGGCTCCCTGACCTGGGAGCGC 180  
Db 13120 AGCGCATTCAGCTCTCTCCGCTGGGGCTCGCTGGGCTCCCTGACCTGGGAGCGC 13179  
Qy 181 GAGCGCGCGCGCGGGGAAGCGCGCCAGACCCCGGGTCCGCCCGAGCAGCTGCG 240  
Db 13180 GAGCGCGCGCGGGGAAGCGCGCCAGACCCCGGGTCCGCCCGAGCAGCTGCG 13239  
Qy 241 CTGTCCGGGCGCAGCGCGGGCTCCAGTGGATTGCGGGGACAGACGCCGAGCGCGCT 300  
Db 13240 CTGTCCGGGCGCAGCGCGGGCTCCAGTGGATTGCGGGGACAGACGCCGAGCGCGCT 13299  
Qy 301 TCCACAGTGGCGGAGGAGCTGGGGACCCGGGACCCGCTCTGCGCCCTTCACTTCCAGCT 360  
Db 13300 TCCACAGTGGCGGAGGAGCTGGGGACCCGGGACCCGCTCTGCGCCCTTCACTTCCAGCT 13359  
Qy 361 CCGCTCTCTCGGCGGAGACCCCGGCGCTCCGACCCCTCCGGGTCCCGGGCCCGGCGCACGCC 420  
Db 13360 CCGCTCTCTCGGCGGAGACCCCGGCGCTCCGACCCCTCCGGGTCCCGGGCCCGGCGCACGCC 13419  
Qy 421 CTTCCGGGCGCTCCAGCGCTCCCTCTCTTTCGGGCGCGCGCGCGCTCTCTCGCGGCG 480  
Db 13420 CTTCCGGGCGCTCCAGCGCTCCCTCTCTTTCGGGCGCGCGCGCGCTCTCTCGCGGCG 13479  
Qy 481 CGAGTTTCAGGACGCTGCTGCTGCGACGCTGGGAAGCCCTGGCCCGGCGCACCC 540  
Db 13480 CGAGTTTCAGGACGCTGCTGCTGCGACGCTGGGAAGCCCTGGCCCGGCGCACCC 13539  
Qy 541 CCGGATGCGCGGCTTCCCGCTGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
Db 13540 CCGGATGCGCGGCTTCCCGCTGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 13599  
Qy 601 GCGAGGTGCTGCGCTGGCCACAGTTCTGTCGGGCGCGCTGGGGCGCCCGAGGCTGGCGGTGG 660

Db 13600 GCGAGGTGCTGCGCTGCGCACAGTTGCTGCGGCGCTTGGGCGCCACAGGGCTGGCGGCTGG 13659  
Qy 661 TGCAGCGCGGGAGACCGCGGCGCTTTCGCGGCGCTGGTGGGCCACAGTGCCTGGTGGCTGC 720  
Db 13660 TGCAGCGCGGGAGACCGCGGCGCTTTCGCGGCGCTGGTGGGCCACAGTGCCTGGTGGCTGC 13719  
Qy 721 CCTGGGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780  
Db 13720 CCTGGGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13779  
Qy 781 TCGCGCTCCGCTGCGGCTTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840  
Db 13780 TCGCGCTCCGCTGCGGCTTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13839  
Qy 841 CAGCGGACTCAGGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900  
Db 13840 CAGCGGACTCAGGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13899  
Qy 901 GCTCGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 960  
Db 13900 GCTCGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 13959  
Qy 961 GGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 1001  
Db 13960 GGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 14000

## RESULT 5

ABSS4997  
ID ABSS4997 standard; DNA; 15418 BP.  
XX AC ABSS4997;  
XX DT 10-DEC-2002 (first entry)  
XX DE Lambda clone containing human TERT genomic insert.  
XX KW Telomerase reverse transcriptase; TERT; replication-conditional virus;  
KW adenovirus replication gene; cancer cell; lung; pancreatic cancer;  
KW medulloblastoma; cervical carcinoma; fibrosarcoma; osteosarcoma;  
KW cytolysis; replication defective adenovirus vector; congenital defect;  
KW proinflammatory; antiinflammatory; heterologous effector gene;  
KW cancer therapy; cytostatic; gene therapy; lambda clone; human; ds.  
XX OS Bacteriophage lambda.  
OS Homo sapiens.  
XX Synthetic.  
FH Key Location/Qualifiers  
FT misc\_feature 1..43  
FT /tag= a  
FT /note= "From Lambda clone"  
FT misc\_feature 44..15375  
FT /tag= b  
FT /note= "Human telomerase reverse transcriptase (hTERT)  
FT sequence including the hTERT promoter and upstream  
FT misc\_feature 15376..15418  
FT /tag= c  
FT /note= "From Lambda clone"  
XX WO200253760-A2.  
XX 11-JUL-2002.  
XX 17-DEC-2001; 2001WO-US048785.  
XX 18-DEC-2000; 2000US-0256418P.  
XX (GERO-) GERON CORP.  
XX Irving JM, Lebkowski JS;

XX WPI; 2002-723123/78.  
XX Novel replication-conditional virus useful for cytolysis of target cells  
XX e.g. cancer cells and preparing a medicament for treating cancer,  
XX comprises heterologous replication element in an adenovirus-based  
XX construct.  
XX Claim 11; Page 26-29; 32pp; English.  
XX The present invention relates to a new replication-conditional virus with  
XX a genome comprising adenovirus replication genes and one or more  
XX heterologous gene(s) that functionally replaces one or more adenovirus  
XX gene(s) required for replication or assembly of the virus. The invention  
XX is useful for killing a cancer cell (such as lung, pancreatic cancer,  
XX medulloblastoma, cervical carcinoma, fibrosarcoma or osteosarcoma),  
XX killing a cell expressing TERT (telomerase reverse transcriptase), and in  
XX preparing a medicament for treating cancer and a condition associated  
XX with increased expression of TERT in affected cells, in a subject. The  
XX invention is also useful for cytolysis of specific target cells. The  
XX adenovirus vector which is useful for producing replication defective  
XX heterologous therapeutic gene to correct a congenital defect, introducing  
XX proinflammatory or antiinflammatory activity, enhancing telomerase  
XX function, and delivering heterologous effector genes that induce killing  
XX of the transduced cells. The invention is more safe for use in cancer  
XX therapy. The present nucleic acid sequence represents the human TERT  
XX sequence contained within a lambda clone sequence of the invention  
XX  
SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1001; DB 6; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 6e-138;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CGTCCGACCTGGAGGAGCGCCCTGGGTCTCGGATCAGGCCAGCGCGCAAGGGTGC 60  
Db 13000 CGTCCGACCTGGAGGAGCGCCCTGGGTCTCGGATCAGGCCAGCGCGCAAGGGTGC 13059  
Qy 61 CAGCAGCTGTTCAGGCGCTCCACATCATGCGCCCTCCCTCGGGTTACCCACAGCT 120  
Db 13060 CAGCAGCTGTTCAGGCGCTCCACATCATGCGCCCTCCCTCGGGTTACCCACAGCT 13119  
Qy 121 AGCGCGATTGACCTCTCTCGCTGGGCGCTCTCGCTGGGCGCTCTGACCTCTGGAGCGC 180  
Db 13120 AGCGCGATTGACCTCTCTCGCTGGGCGCTCTCGCTGGGCGCTCTGACCTCTGGAGCGC 13179  
Qy 181 GAGCGCGCGCGCGCGGGAAGCGCGGCCAGACCCCGCGGTCCGCGGAGCAGCTGC 240  
Db 13180 GAGCGCGCGCGCGCGGGAAGCGCGGCCAGACCCCGCGGTCCGCGGAGCAGCTGC 13239  
Qy 241 CTGTGCGGCGCAGCGCGGCTCCAGTGGATTGCGGGGACAGAGCCCGAGCGCGCT 300  
Db 13240 CTGTGCGGCGCAGCGCGGCTCCAGTGGATTGCGGGGACAGAGCCCGAGCGCGCT 13299  
Qy 301 TCCACATGCGGAGGAGCTGGGACCCCGCGCCCGCTCCGCGGTCCCGCGGCGCGCC 360  
Db 13300 TCCACATGCGGAGGAGCTGGGACCCCGCGCCCGCTCCGCGGTCCCGCGGCGCGCC 13359  
Qy 361 CCGCTCTCTCCGCGGACCCCGCGCCCGCTCCGCGGTCCCGCGGCGCGCCCGCGCC 420  
Db 13360 CCGCTCTCTCCGCGGACCCCGCGCCCGCTCCGCGGTCCCGCGGCGCGCCCGCGCC 13419  
Qy 421 CCTCGGCGCTCCGAGCGCTCCCTCTCTTTCGCGGCGCGCGCTCTCTCTCGCGCG 480  
Db 13420 CCTCGGCGCTCCGAGCGCTCCCTCTCTTTCGCGGCGCGCGCTCTCTCTCGCGCG 13479  
Qy 481 CGAGTTTCAGGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540  
Db 13480 CGAGTTTCAGGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 13539  
Qy 541 CCGGATGCGCGCGCTCCCGCGCTCCGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600

Db 13540 CCGGATGCGCGCGCTCCCGCTGCGAGCGGTGGCTCCCTGCTGGCAGCACTACC 13599  
Qy 601 GCAGAGTGTCTCCGCTGGCCACAGTTCTGTCGGCGCCCTGGGGCCCCCAGAGCTGCGCGTGG 660  
Db 13600 GCGAGGTGTCTCCGCTGGCCACAGTTCTGTCGGCGCCCTGGGGCCCCCAGAGCTGCGCGTGG 13659  
Qy 661 TGACGCGCGGGGACCCCGCGGCTTTTCGCGCGCTGTGGCCCACTGCTGTGTGTGCTGTC 720  
Db 13660 TGCAGCGCGGGGACCCCGCGGCTTTTCGCGCGCTGTGGCCCACTGCTGTGTGTGCTGTC 13719  
Qy 721 CCTGGGACGACAGCGCCCGCCCGCGCCCTCTCTTCGCGCAGGTGGGCTCCCGCGGG 780  
Db 13720 CCTGGGACGACAGCGCCCGCCCGCGCCCTCTCTTCGCGCAGGTGGGCTCCCGCGGG 13779  
Qy 781 TCGCGCTCCGCTGGGTGTAGGGCGCGCGCGGGGGAACCGAGCAGTCGCGAGAGCAGCG 840  
Db 13780 TCGCGCTCCGCTGGGTGTAGGGCGCGCGCGGGGGAACCGAGCAGTCGCGAGAGCAGCG 13839  
Qy 841 CAGCGCACTCAGGCGCTTCCCGCGCAGGTCTCTGCTGAAGAGCTGTGGCCCGAGT 900  
Db 13840 CAGCGCACTCAGGCGCTTCCCGCGCAGGTCTCTGCTGAAGAGCTGTGGCCCGAGT 13899  
Qy 901 GCTGCAGAGGTGTGCGAGCGCGCGGGAAGACGTCTGCGCTTCGGCTTCGCGCTGCT 960  
Db 13900 GCTGCAGAGGTGTGCGAGCGCGCGGGAAGACGTCTGCGCTTCGCGCTTCGCGCTGCT 13959  
Qy 961 GGACGGGCGCGCGGGGCGCCCGCGAGGCTTCACCA 1001  
Db 13960 GGACGGGCGCGCGGGGCGCCCGCGAGGCTTCACCA 14000

RESULT 6

AAL38595  
ID AAL38595 standard; DNA; 15418 BP.  
XX  
AC AAL38595;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE DNA of plasmid pGRN144 containing human hTERT gene.  
XX  
KW Anticonvulsant; cerebroprotective; vasotropic; nootropic; stem cell;  
KW neuroprotective; antiparkinsonian; antiinflammatory; undifferentiated;  
KW cardiant; transcriptional control element; human embryonic; tissue graft;  
KW regenerative medicine; tissue reconstruction; neural progenitor cell;  
KW nerve system; epilepsy; stroke; ischaemia; Huntington's disease;  
KW Parkinson's disease; multiple sclerosis; leukodystrophy; neuritis;  
KW hepatocyte; liver damage; cardiomyocyte; cryoinjury; cardiac muscle;  
KW pGRN144; human hTERT gene; chimeric; ds.  
XX  
OS Homo sapiens.  
OS Unidentified.  
OS Chimeric.  
XX  
PN WO200242445-A2.  
XX  
PD 30-MAY-2002.  
XX  
XX 26-NOV-2001; 2001WO-US044309.  
XX  
XX 27-NOV-2000; 2000US-0253357P.  
PR 27-NOV-2000; 2000US-0253443P.  
PR 13-FEB-2001; 2001US-00783203.  
XX  
XX (GERO-) GERON CORP.  
XX  
XX Gold JD, Lebrowski JS;  
XX  
XX WPI; 2002-479952/51.  
XX  
XX Depleting a cell e.g., human embryonic stem cell population of  
PT undifferentiated stem cells (UC) for use in regenerative medicine  
PT comprises genetically altering UC in a population to express nucleic acid

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

encoding a lethal product.

Example 9; Page 62-66; 67pp; English.

The invention relates to a system for depleting a cell population of undifferentiated stem cells, by introducing nucleic acids of structure P-X, where X is a nucleic acid encoding product that is lethal to a cell in which it is expressed; or renders a cell in which it is expressed susceptible to the lethal effect of an external agent, and P is a transcriptional control element causing X to be preferentially expressed in the undifferentiated stem cells. The system is used for depleting a cell population (preferably, human embryonic stem cells) of undifferentiated stem cells, a population of differentiated cells is useful in regenerative medicine, and for preparing antibodies and cDNA libraries that are specific for a differentiated phenotype. The cell populations are also useful for drug screening and therapeutic applications. The differentiated cells are useful for tissue reconstitution or regeneration in a human patient in need of treatment. The cells are administered in a manner that permits to graft to the intended tissue side and reconstitute or regenerate the functionally deficient area. The neural progenitor cells are useful for treating acute or chronic damage to the nerve system e.g. epilepsy, stroke, ischaemia, Huntington's disease, Parkinson's disease, multiple sclerosis, leukodystrophies, neuritis, etc. The hepatocytes and hepatocyte precursors are useful for assessing animal models for ability to repair liver damage. The cardiomyocyte population is useful for assessing animal models for cryoinjury, regenerating cardiac muscle and to treat insufficient cardiac function. This polynucleotide sequence represents the DNA of plasmid pGRN144 containing the human hTERT gene relating to the invention

Sequence 15418 BP; 4519 A; 3797 C; 3764 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 1001; DB 6; Length 15418;

Best Local Similarity 100.0%; Pred. No. 6e-138;

Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCGAGGAGGTCGCGC 60  
Db 13000 CGTCCGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCGAGGAGGTCGCGC 13059  
Qy 61 CAGCACCTGTTCCAGGGGCTCCACATATGCCCCCTCCCTGGGTATACCCACAGCCT 120  
Db 13060 CAGCACCTGTTCCAGGGGCTCCACATATGCCCCCTCCCTGGGTATACCCACAGCCT 13119  
Qy 121 AGGCCGATTGACCTCTCTCCGTGGGGCCCTCGCTGGCGTCCCTGCACCTGGGAGCGC 180  
Db 13120 AGGCCGATTGACCTCTCTCCGTGGGGCCCTCGCTGGCGTCCCTGCACCTGGGAGCGC 13179  
Qy 181 GAGCGGGCGCGGGGGAAGCGCGGCCAGACCCCGGGTCCGCCGAGCAGCTGCG 240  
Db 13180 GAGCGGGCGCGGGGGAAGCGCGGCCAGACCCCGGGTCCGCCGAGCAGCTGCG 13239  
Qy 241 CTGTGCGGGCCAGCGCGGGCTCCAGTGGATTGCGGGCACAGACGCCAGGACCGCGCT 300  
Db 13240 CTGTGCGGGCCAGCGCGGGCTCCAGTGGATTGCGGGCACAGACGCCAGGACCGCGCT 13299  
Qy 301 TCCACAGTGGCGAGGAGCTGGGGACCCCGGGCACCCGTCTCTGCCCCCTTCACCTTCCAGCT 360  
Db 13300 TCCACAGTGGCGAGGAGCTGGGGACCCCGGGCACCCGTCTCTGCCCCCTTCACCTTCCAGCT 13359  
Qy 361 CGCGCTCTCCCGCGGAGACCCCGCGCCCGTCCGACCCCTCCCGGTCCCGGCCAGGCC 420  
Db 13360 CGCGCTCTCCCGCGGAGACCCCGCGCCCGTCCGACCCCTCCCGGTCCCGGCCAGGCC 13419  
Qy 421 CTTCCGGGGCTCCCGAGCCCTCCCTTCTTTTCGGGGCCCGCCCTCTCTCCGGCGC 480  
Db 13420 CTTCCGGGGCTCCCGAGCCCTCCCTTCTTTTCGGGGCCCGCCCTCTCTCCGGCGC 13479  
Qy 481 CGAGTTTCAGGCGAGCTGCGTCTCTGTCGCGCAGTGGGAGCCCTGCGCCCGGCCACCC 540  
Db 13480 CGAGTTTCAGGCGAGCTGCGTCTCTGTCGCGCAGTGGGAGCCCTGCGCCCGGCCACCC 13539



Qy 601 GCGAGGTGCTCCGCTGCGCACAGTTCTGTCGGCGGCTTGGGGCCCCAGGGCTGGCGGCTGG 660  
Db |||||  
13600 GCGAGGTGCTCCGCTGCGCACAGTTCTGTCGGCGGCTTGGGGCCCCAGGGCTGGCGGCTGG 13659  
Qy 661 TGCAGCGCGGGAGACCGCGCGCTTTCCGCGCGCTGTGTGGGCCAGTGCCTGGTGTGCTGTC 720  
Db |||||  
13660 TGCAGCGCGGGAGACCGCGCGCTTTCCGCGCGCTGTGTGGGCCAGTGCCTGGTGTGCTGTC 13719  
Qy 721 CTTGGGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780  
Db |||||  
13720 CTTGGGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13779  
Qy 781 TCGCGCTGCTCGGCTGGGCTTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840  
Db |||||  
13780 TCGCGCTGCTCGGCTGGGCTTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13839  
Qy 841 CAGCGGACTCAGGCGCGCTTCCCGCGCAGGTGTCTGCTGCTGAAGAGCTGTGTGGCCCGAGT 900  
Db |||||  
13840 CAGCGGACTCAGGCGCGCTTCCCGCGCAGGTGTCTGCTGCTGAAGAGCTGTGTGGCCCGAGT 13899  
Qy 901 GCTCAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960  
Db |||||  
13900 GCTCAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13959  
Qy 961 GGAGCGGGCGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1001  
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13960 GGAGCGGGCGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14000

RESULT 8  
ADU82631

ID ADU82631 standard; DNA; 5491 BP.

AC ADU82631;

XX 10-FEB-2005 (first entry)

XX Human hTERT gene nucleotide sequence.

XX Gene expression; transcription; TERT; telomerase reverse transcriptase;  
KW cancer therapy; cyclostatic; CNS; respiratory; anti-HIV; antianemic;  
KW antisickling; hemostatic; antidiabetic; cardiant; antiinflammatory;  
KW antirheumatic; antiarthritic; neuroprotective; antiasthmatic; vasotropic;  
KW gene therapy; apoptosis stimulator; cancer; gene; ds.  
XX Homo sapiens.

XX Key Location/Qualifiers  
FH 3415..3633  
FT /\*tag= a  
FT /product= "telomerase reverse transcriptase fragment"  
FT /partial

XX W02004099377-A2.

XX 18-NOV-2004.

XX 30-APR-2004; 2004WO-US013487.

XX 01-MAY-2003; 2003US-0467171P.

XX (MUSC-) MUSC FOUND RES DEV.

XX Dong J, Rubinchik S, Woraratanadham J;

XX WPI; 2004-805118/79.

XX P-PSDB; ADU82632.

XX GENBANK; AB016767.

XX New expression vector comprising a first expression cassette with a first  
PT coding region that encodes a transcriptional activating factor (TAF),  
PT useful in treating cancer, AIDS, hemophilia, diabetes and asthma.

PS The invention relates to an expression vector comprising a first  
XX expression cassette having a first coding region that encodes a  
CC transcriptional activating factor (TAF), and a second expression cassette  
CC comprising a second coding region that encodes a selected polypeptide.  
CC The expression vector further comprises a first expression cassette  
CC having a first coding region that encodes a transcriptional activating  
CC factor (TAF), the first coding region being positioned under the  
CC transcriptional control of a first promoter comprising a tissue specific  
CC regulatory element (TSRE), and a TAF binding site (TBS), and a second  
CC expression cassette comprising a second coding region that encodes a  
CC selected polypeptide, the second coding region being positioned under the  
CC transcriptional control of a second promoter comprising a TSRE and a TBS,  
CC or a TBS. The expression vector further comprises a third coding region  
CC that encodes a first transcriptional silencer (TSI), the third coding  
CC region being positioned under the transcriptional control, a third  
CC promoter comprising a TSRE and a TAB, and a fourth expression cassette  
CC comprising a fourth coding region that encodes a second TSI, the fourth  
CC coding region being positioned under the transcriptional control of a  
CC fourth promoter that is negatively regulated by the first TSI, where the  
CC first, second and third promoters are negatively regulated by the second  
CC TSI. The selected polypeptide is a therapeutic polypeptide, such as an  
CC anti-cancer polypeptide that is a tumor suppressor, and inducer of  
CC apoptosis, and cell cycle regulator, a toxin, or an inhibitor of  
CC angiogenesis, and an enzyme, a cytokine, a hormone, a tumor antigen, a  
CC human antigen or a pathogen antigen. The selected polypeptide is  
CC essential for vector replication, where the vector is an adenoviral  
CC vector. The expression vector is useful in methods for treating cancer  
CC and further comprises a selectable or screenable marker. The methods and  
CC compositions of the present invention are useful in the fields of  
CC molecular biology and gene therapy, particularly to the combined spatial  
CC and quantitative regulation of transgene expression in eukaryotic cells,  
CC and in treating cancer including breast cancer, ovarian cancer, fallopian  
CC tube cancer, cervical cancer, uterine cancer, bladder cancer, liver cancer,  
CC stomach cancer, lung cancer, lymphoid cancer, brain cancer, thyroid  
CC cancer, head and neck cancer, skin cancer or leukemia. The cancer is a  
CC recurrent cancer, a metastatic cancer or a drug resistant cancer. The  
CC methods and compositions can also be used in treating cystic fibrosis,  
CC AIDS, sickle cell anemia, rheumatoid arthritis, multiple sclerosis, asthma  
CC inflammatory disorders, hemophilia, diabetes, heart disease,  
CC and restenosis. The present sequence represents a human telomerase  
CC reverse transcriptase (hTERT) gene nucleotide sequence, the promoter  
CC fragment can be used in the vectors of the invention.  
XX

SQ Sequence 5491 BP; 954 A; 1729 C; 1677 G; 1131 T; 0 U; 0 Other;

Query Match 99.8%; Score 999.4; DB 13; Length 5491;  
Best Local Similarity 99.9%; Pred. No. 1.2e-137;  
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTCCGACCTGGAGGAGCCCTGGGTTCTCCGATCAGGCGAGCGGCAAGGTTCCGCCG 60  
Db |||||  
2870 CGTCCGACCTGGAGGAGCCCTGGGTTCTCCGATCAGGCGAGCGGCAAGGTTCCGCCG 2929  
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Db |||||  
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Db |||||  
2990 AGGCCGATTGCGACTCTCTCCGCTGGGGCCCTCGCTGGCGCTCCCTGCACCTGGGAGCGC 3049  
Qy 181 GAGCGCGCGCGCGGGGGAAGCGCGGCCAGACCCCGGGTCCGCCGAGCAGCTGCG 240  
Db |||||  
3050 GAGCGCGCGCGCGGGGAAGCGCGGCCAGACCCCGGGTCCGCCGAGCAGCTGCG 3109  
Qy 241 CTCTCGGGGCGAGCGGGCTCCAGTGGATTGCGGGGACAGCGCCAGGACCGCGCT 300  
Db |||||  
3110 CTCTCGGGGCGAGCGGGGCTCCAGTGGATTGCGGGGACAGCGCCAGGACCGCGCT 3169  
Qy 301 TCCACGTGGCGAGGAGACTGGGGACCCGGGGACCCGCTCCTGCGCCCTTTCACCTTCCAGCT 360

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Db 3170 CCCACGTGGCGGAGGACTGGGACCCGGGACACCGTCTCTGCCCCCTTCACCTTCCAGCT 3229
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Db 3230 CCGCTCTCTCGCGCGAGACCCCGCCGCTCCGACCCCTCCCGGTCCTCCGCGCCAGCC 3289
Qy 421 CCTCGGCGCTCCAGCCCTCCCTTCTCTTTCGCGGCGCCCGCCCTCTCTCGCGCG 480
Db 3290 CCTCGGCGCTCCAGCCCTCCCTTCTCTTTCGCGGCGCCCGCCCTCTCTCGCGCG 3349
Qy 481 CGAGTTTCAGGACGCTGCTCTGTCTGCGACAGTGGAGAGCCCTGCGCCCGGCCACCC 540
Db 3350 CGAGTTTCAGGACGCTGCTCTGTCTGCGACAGTGGAGAGCCCTGCGCCCGGCCACCC 3409
Qy 541 CCGGATGCGCGCGCTCCCGCTGCGAGCGGCTGCGCTCTCTGCGGAGCCACTACC 600
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Qy 601 GCGAGGTGCTGCTGCGCTGCGCACAGTTCTGCGGCGCTGCGGCGCCAGGCGCTGGCGGTGG 660
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Qy 661 TGCAGCGCGGAGACCCCGCGCTTTTCCGCGCGCTGCTGCGGCGCTGCTGCTGCTGCTGCTG 720
Db 3530 TGCAGCGCGGAGACCCCGCGCTTTTCCGCGCGCTGCTGCGGCGCTGCTGCTGCTGCTGCTG 3589
Qy 721 CCTGGGAGCGACGCGCGCCCGCCCGCGCTCTCTTCCGCGAGTGGGCTTCCCGGGG 780
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Qy 781 TCGCGCTCGCGCTGGGCTTGAAGGCGCGCGCGGCGGAGACGACGACATGCGGAGAGAGCG 840
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Qy 841 CAGCGGACTCAGGCGCTTCCCGCGAGGTGCTCTGCTGAAGGAGCTGGTGGCCCGAGT 900
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Qy 901 GCTCAGAGCTGTCGAGCGCGCGCGGAGAACTGCTGCGCTTCCGCTTCCGCGTCTGCT 960
Db 3770 GCTCAGAGCTGTCGAGCGCGCGCGGAGAACTGCTGCGCTTCCGCTTCCGCGTCTGCT 3829
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RESULT 9
AAS96607
ID AAS96607 standard; DNA; 51552 BP.
XX
AC AAS96607;
XX
DT 09-APR-2002. (first entry)
XX
DE DNA encoding human telomerase reverse transcriptase (TERT) #1.
XX
KW Telomerase reverse transcriptase; TERT; cytosolic; apoptosis;
KW cell growth inhibitor; antisense oligonucleotide; antisense technology;
KW ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT exon 1. .11492
FT /tag= a
FT /number= 1
FT CDS 11274. .47813
FT /tag= b
FT /product= "TERT"
FT /note= "Telomerase reverse transcriptase"
FT intron 11493. .11596
FT
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FT /tag= e
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FT /tag= f
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FT intron 21763. .23851
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FT exon 23852. .24032
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FT /number= 4
FT intron 24033. .24719
FT /tag= i
FT exon 24720. .24899
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/\*tag= ae  
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47710. .50544  
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FT /number= 16

WO200188198-A1.

22-NOV-2001.

15-MAY-2001; 2001WO-US015774.

16-MAY-2000; 2000US-00572423.

07-DEC-2000; 2000US-00733294.

(ISIS-) ISIS PHARM INC.

Monia BP, Gaarde WA, Freier SM, Wanciewicz E;

WPI; 2002-075321/10.

P-PSDB; AAU72735.

XX New compound targeted to nucleic acid molecule encoding telomerase  
PT transcriptase (TERT), which specifically hybridizes with and inhibits  
PT expression of TERT, useful for modulating apoptosis and inhibiting cell  
PT growth.

XX Example 19; Page 112-138; 154pp; English.

CC The invention describes a compound, 8-50 nucleobases in length targeted  
CC to a nucleic acid molecule encoding human TERT (telomerase reverse  
CC transcriptase), where the compound specifically hybridizes with and  
CC inhibits the expression of TERT. A series of oligonucleotides were  
CC designed to target different regions of the human TERT RNA. These were 20  
CC nucleotides in length and composed of a central gap region consisting of  
CC ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by  
CC five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-  
CC MOE) nucleotides. The compounds were analysed for their effect on human  
CC TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction  
CC (PCR). The compound is useful for inhibiting the expression of TERT in  
CC cells or tissues, for treating a human having disease or condition  
CC associated with TERT, for modulating apoptosis, for inhibiting cell  
CC growth (preferably, cancer cell growth), in antisense therapy and for  
CC diagnostics and therapeutics. This sequence encodes human telomerase  
CC reverse transcriptase (TERT) #1, and is used to create antisense  
CC oligonucleotides which modify TERT expression, described in the method of  
CC the invention

XX SQ Sequence 51552 BP; 10709 A; 13313 C; 15370 G; 12158 T; 0 U; 2 Other;

Query Match 99.8%; Score 999.4; DB 6; Length 51552;  
Best Local Similarity 99.9%; Pred. No. 8.4e-138;  
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTCCGACCTGGAGGCGAGCCCTGGGTCTCCGGATCAGGCGCAGCGGCAAGGGTCCCG 60  
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Db 10849 AGCCCGATTTCGACCTCTCTCCGCTGGGGCCCTCGCTGGGCTCCCTGCACCTCGGAGCGC 10908  
Qy 181 GAGCGCGCGCGCGGCGGGAAGCGCGGCCAGACCCCGGGTCCGCCCGAGAGCTGCG 240  
Db 10909 GAGCGCGCGCGCGGCGGGAAGCGCGGCCAGACCCCGGGTCCGCCCGAGAGCTGCG 10968  
Qy 241 CTGTCCGGGCGCAGGCCGGGCTCCAGTGGATTCCGGGGCAACAGACCCAGAGCCCGCGCT 300  
Db 10969 CTGTCCGGGCGCAGGCCGGGCTCCAGTGGATTCCGGGGCAACAGACCCAGAGCCCGCGCT 11028  
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Db 11029 CCCACAGTGGCGGAGGAGACTGGGGACCCCGGGACCCGCTCTGCTGCCCTTCACTTCCAGCT 11088  
Qy 361 CGGCTCTCTCCGCGCGGACCCCGCCCGTCCCGACCCCTCCCGGGTCCCGGGCCAGCCCC 420  
Db 11089 CGGCTCTCTCCGCGCGGACCCCGCCCGTCCCGACCCCTCCCGGGTCCCGGGCCAGCCCC 11148  
Qy 421 CTTCCGGGCGCTCCAGAGCCCTCCCTTCTTTCGGGGCCCGCCCTCTCTCTGGGGCG 480  
Db 11149 CTTCCGGGCGCTCCAGAGCCCTCCCTTCTTTCGGGGCCCGCCCTCTCTCTGGGGCG 11208  
Qy 481 CGAGTTTTCAGGCGAGCGCTGCTGCTGCGCACGCTGGGAAGCCCTGGGCCCCGACCC 540  
Db 11209 CGAGTTTTCAGGCGAGCGCTGCTGCTGCGCACGCTGGGAAGCCCTGGGCCCCGACCC 11268  
Qy 541 CGCGGATGCGCGCGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCGGAGCAGCTPACC 600  
Db 11269 CGCGGATGCGCGCGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCGGAGCAGCTPACC 11328  
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Qy 841 CAGGCGACTTCAGGGCGCTTCCCGCGCAGGTGTCTGCTGAAGGAGCTGGTGGCCCGAGT 900  
Db 11569 CAGGCGACTTCAGGGCGCTTCCCGCGCAGGTGTCTGCTGAAGGAGCTGGTGGCCCGAGT 11628  
Qy 901 GCTGCAGAGGCTGTGCGAGCGCGCGGCGAAGACGCTGCTGCTTCCGGCTTCGCGCTGCT 960  
Db 11629 GCTGCAGAGGCTGTGCGAGCGCGCGGCGAAGACGCTGCTGCTTCCGGCTTCGCGCTGCT 11688  
Qy 961 GGAAGGGGCGCGGGGGGCCCCCGGAGGCTTCAACACCA 1001  
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RESULT 10

AAV16979

ID AAV16979 standard; DNA; 4335 BP.

XX AC

AAV16979;

XX AC

13-AUG-1998 (first entry)

XX Human telomerase reverse transcriptase genomic clone.

DE Human; telomerase reverse transcriptase; hTERT; TERT; diagnosis; prognosis;

KW cell proliferation; cancer; ageing; ribonucleoprotein; ss.







ADV23865;  
AC  
XX 24-FEB-2005 (first entry)  
DT  
XX  
XX Human hTERT gene 5' flanking region, intron 1 and exon 1, SEQ ID 1.  
DE  
XX Cytostatic; Gene therapy; cancer; telomerase;  
KW telomerase reverse transcriptase; hTERT; enzymes; gene; ds.  
XX  
XX Homo sapiens.  
OS  
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FT /note= "This region is specifically claimed in Claims 4  
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FT /note= "This region is specifically claimed in Claims 4  
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FT /note= "This region is specifically claimed in Claims 4  
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FT /note= "This region is identical to the Hepatitis B virus  
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FT /note= "This region is specifically claimed in Claims 4  
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FT /tag= j  
FT /note= "This region is responsible for full promoter  
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FT exon

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XX US2004248246-A1.  
XX  
XX 09-DEC-2004.  
PD  
XX 05-JUN-2003; 2003US-00456830.  
XX  
XX 05-JUN-2003; 2003US-00456830.  
PR  
XX (USAS ) NASA US NAT AERO & SPACE ADMIN.  
XX  
XX Horikawa I, Barrett JC;  
PI  
XX WPI: 2005-020562/02.  
XX P-PSDB; ADV23866.  
DR  
XX  
XX New regulatory control sequence comprising a promoter that directs  
FT differential expression of an operably linked heterologous nucleic acid  
FT sequence in a first cell type, useful for preparing a composition for  
FT treating cancer.  
XX  
XX Claim 4; SEQ ID NO 1; 46pp; English.  
PS  
XX The present invention relates to a new regulatory control sequence (I)  
CC which is useful for preparing a composition for treating cancer. (I)  
CC comprises: (a) a promoter that directs differential expression of an  
CC operably linked heterologous nucleic acid sequence (e.g. cytotoxins) in a  
CC first cell type as compared to a second cell type, where the first cell  
CC type is a telomerase-positive or a cancer cell and the second cell type  
CC is a telomerase-negative or a normal somatic cell; and (b) at least one  
CC exogenous E-box element linked in cis with the promoter sequence and that  
CC enhances the differential expression directed by the promoter. The  
CC promoter is preferably a human telomerase reverse transcriptase (hTERT)  
CC promoter. hTERT is the catalytic subunit of the human telomerase complex,  
CC which is responsible for the replication of telomeres. E-box elements are  
CC regulatory control elements that are recognized by numerous transcription  
CC factors, e.g. transcription factors from the basic helix-loop-helix  
CC structural family. Differential E-box-mediated repression of hTERT gene  
CC promoter activity has been discovered, where repression occurs in normal  
CC cells but not in many cancer cells. By linking E-box elements in cis with  
CC TERT transcriptional regulatory sequences, the expression of heterologous  
CC sequences operably linked to the TERT transcriptional regulatory  
CC sequences can be preferentially suppressed in normal cells. However, the  
CC expression of such heterologous sequences is not suppressed in cancer  
CC cells. The present sequence is the nucleotide sequence is the 5'-flanking  
CC region, exon 1 and intron 1 of the hTERT gene, used to illustrate the  
XX invention.  
XX  
XX Sequence 4293 BP; 817 A; 1278 C; 1234 G; 961 T; 0 U; 3 Other;  
SQ  
Query Match 86.7%; Score 867.6; DB 14; Length 4293;  
Best Local Similarity 99.9%; Pred. NO. 2.2e-118;  
Matches 867; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTCGGACCTGGAGGCGCCCTGGCTCTCGGATCAGGCCGCGCCAAAGGTCGCG 60  
DB 3426 CGTCGGACCTGGAGGCGCCCTGGCTCTCGGATCAGGCCGCGCCAAAGGTCGCG 3485  
QY 61 CACGACCTGTTCCAGGCGCTCCACATCATGCGCCCTCCCTCGGGTTACCCACAGCT 120  
DB 3486 CACGACCTGTTCCAGGCGCTCCACATCATGCGCCCTCCCTCGGGTTACCCACAGCT 3545  
QY 121 AGGCGGATTCGACCTCTCTCCGCTGGGCGCCCTCGCTGGCGTCCCTGCACCTGGAGCGC 180  
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Qy 301 TCCACGCTGCGGAGGAGCTGGGACCCGGGACCCCGTCTGCTCCCTTCCAGCT 360
Db 746 TCCACGCTGAGGAAAAAATAAAACCCGAAACCCCGTCTTACCCCTTCCAACT 687
Qy 361 CCGCTCTCTCCGCGGACCCCGCCGCTCCGACCCCTCCCGGCTCCCGGCGCCAGCC 420
Db 686 CCGCTCTCTCCGCGGAAACCCCGCCGCTCCGACCCCTCCGAAATCCCGACCCACCC 627
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## RESULT 15

AE18046/c  
ID AE18046 standard; DNA; 7928 BP.

XX AC AE18046;

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XX DE DE 11-AUG-2005 (first entry)

XX DE DE 11-AUG-2005 (first entry)

XX Widschwendter M;

XX WPI; 2005-396129/40.

XX Detecting, differentiating, and prognosing a gynecological cell  
proliferative disorder by obtaining a cervicovaginal secretion specimen  
from an individual and determining the methylation status of at least one  
or more CpG positions.

XX Claim 8; SEQ ID NO 32; 163pp; English.

XX The invention relates to a method of detecting, differentiating, and  
prognosing a gynecological cell proliferative disorder comprising  
obtaining a cervicovaginal secretion specimen from an individual,  
determining the methylation status of at least one or more CpG positions,  
and/or prognosing a gynecological cell proliferative disorder in the  
individual. The method is useful for detecting, differentiating, and  
prognosing a gynecological cell proliferative disorder, e.g. dysplasia or  
low-grade squamous intraepithelial lesions, high-grade squamous  
intraepithelial lesions, cervical cancer, endometrial cancer, or grade 1  
to 3 cervical intraepithelial neoplasia. The present sequence represents  
a converted gynecological cell proliferative disorder related gene.

XX Sequence 7928 BP; 1629 A; 535 C; 2410 G; 3354 T; 0 U; 0 Other;

Query Match 62.9%; Score 629.8; DB 14; Length 7928;  
Best Local Similarity 76.8%; Pred. No. 1.1e-83;  
Matches 769; Conservative 0; Mismatches 232; Indels 0; Gaps 0;

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1001	100.0	4321	6	AR390473 Sequence
c 3	1001	100.0	7928	6	CS105926 Sequence
4	1001	100.0	15332	8	AF121948 Homo sapi
5	1001	100.0	15418	6	AR342806 Sequence
6	1001	100.0	15418	6	AR490112 Sequence
7	1001	100.0	15418	6	AR576878 Sequence
8	1001	100.0	15418	6	AX453025 Sequence
9	1001	100.0	15418	6	AX498409 Sequence
10	1001	100.0	15418	6	AX504952 Sequence
11	1001	100.0	92564	8	AY007685 Homo sapi
c 12	1001	100.0	161252	14	AC114955
13	1001	100.0	202305	8	AC114291
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VERSION CQ972301.1 GI:57163511  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Eichler-Wertens,M., Piepenbrock,C. and Olek,A.  
TITLE Method of analyzing cytosin methylation status of  
cancer-testis-antigens for individualised immunotherapy  
JOURNAL Patent: EP 1491639-A 44 29-DEC-2004;  
EpiGenomics AG (DE)  
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Location/Qualifiers  
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VERSION AR390473.1 GI:40112397
KEYWORDS
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4321)
AUTHORS Morin,G.B. and Andrews,W.H.
TITLE Promoter for telomerase reverse transcriptase
JOURNAL Patent: US 6610839-A 6 26-AUG-2003;
Geron Corporation; Menlo Park, CA
FEATURES
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Db |||||
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Qy	601	GCAGAGTGCTGC	CGCTGGCCACACGTTTCGTGGGGCGCTTGGGGCCCAAGGGCTGGCGGCTGG	660			
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Db	5633	CAGCGCACTCAG	GGCGCTTCCCCCGCAGGTGTCTTCCTTCGCGCGCTGGTGGCGCTTGGTGGCGG	5574			
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Db	5573	GCTGCAGAGCTGT	GCAGCGCGCGCGGCGAAGAACGTCGTGGCGCTTGGCGCTTGGCGCTGGCT	5514			
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Db	5513	GGACGGGGCGCG	GGGGGGCCCCCGCGAGGCGCTTCACCA	5473			
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DEFINITION	Homo sapiens telomerase reverse transcriptase (TERT) gene, partial cds.						
ACCESSION	AF121948	1 GI:4580662					
VERSION	AF121948.1						
KEYWORDS							
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.						
AUTHORS	1 (bases 1 to 15332) Greenberg, R.A., O'Hagan, R.C., Deng, H., Xiao, Q., Han, S.R., Adams, R.R., Lichtsteiner, S., Chin, L., Morin, G.B. and DePinho, R.A.						
TITLE	Telomerase reverse transcriptase gene is a direct target of c-Myc but is not functionally equivalent in cellular transformation						
JOURNAL	Oncogene 18 (5), 1219-1226 (1999)						
PUBMED	10022128						
REFERENCE	2 (bases 1 to 15332) Morin, G.B., Carlos, R. and Adams, R.R.						
AUTHORS	Direct Submission						
TITLE	Submitted (21-JAN-1999) Genon Corporation, 230 Constitution Drive, Menlo Park, CA 94025, USA						
JOURNAL							
FEATURES	Location/Qualifiers						
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ORIGIN

Query Match 100.0%; Score 1001; DB 8; Length 15332;  
Best Local Similarity 100.0%; Pred. No. 3.8e-98;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CAGCACCTGTTCACAGGCTCCACATCATATGCGCCCTCCCTCGGGTTACCCACAGCCT 120  
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Qy 121 AGGCCGATTGACCTCTTCGCTGGGGCCCTCGCTGGCGTCCCTGCACCTGGAGCGC 180  
Db 13077 AGGCCGATTGACCTCTTCGCTGGGGCCCTCGCTGGCGTCCCTGCACCTGGAGCGC 13136

Qy 181 GAGCGCGCGCGCGGGGAGCGCGGCCAGACCCCGCGGTCCGCGGAGCAGCTGCG 240  
Db 13137 GAGCGCGCGCGCGGGAGCGCGGCCAGACCCCGCGGTCCGCGGAGCAGCTGCG 13196

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Qy 361 CGGCTCTCTCGCGCGAGACCCCGCCGCTCCGACCCCTCCCGGCTCCCGGCGCCAGCCC 420  
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Qy 421 CCTCGGGCCCTCCAGCGCTCCCTCTCTTTCGGCGGCGCCGCGCTCTCTCGCGCG 480  
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Qy 481 CGAGTTTCAGGACAGCGTGGTCTGCTGCGACGCTGGGAGCCCTGGCCCGCGCCACCC 540  
Db 13437 CGAGTTTCAGGACAGCGTGGTCTGCTGCGACGCTGGGAGCCCTGGCCCGCGCCACCC 13496

Qy 541 CCGCGATCCCGCGCGCTCCCGCTGCCAGCGCTGCGCTCCCTGCTGCGAGCCACTACC 600  
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Qy 601 GCGAGGTGCTGCCCTGGCGACAGTTGCTGCGCGCCCTGGGGCCCGAGGGCTGGCGGTG 660  
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Qy 721 CTTGGGACGACAGCGCCCGCCCGCCCTCTCTTTCGCGAGGTGGGCTCCCGCGGG 780  
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Qy 841 CAGCGGACTCAGGGCGCTTCCCCCGCAGGTGCTCTGCTGGAAGGAGCTGTGGGCCGAGT 900

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Qy 961 GGAAGGGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1001

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RESULT 5

AR342806

LOCUS AR342806 15418 bp DNA linear PAT 17-AUG-2003

DEFINITION Sequence 1 from patent US 6576464.

ACCESSION AR342806

VERSION AR342806.1 GI:33738009

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15418)

AUTHORS Gold, J.D. and Lebkowski, J.S.

TITLE Methods for providing differentiated stem cells

JOURNAL Patent: US 6576464-A 1 10-JUN-2003;

GERON Corporation; Menlo Park, CA

FEATURES

Location/Qualifiers

source 1.15418

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 1001; DB 6; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 3.8e-98;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 AGCGCGATTGCACTCTCTCGCTGGGGCCCTCGCTGGCGCTCCCTGCACTGAGGAGCGC 180  
Db 13120 AGCGCGATTGCACTCTCTCGCTGGGGCCCTCGCTGGCGCTCCCTGCACTGAGGAGCGC 13179

Qy 181 GAGCGCGCGCGCGGGGAGCGCGGCCAGACCCCGGGTCCGCCGCGAGCAGCTGCG 240  
Db 13180 GAGCGCGCGCGGGGAGCGCGGCCAGACCCCGGGTCCGCCGCGAGCAGCTGCG 13239

Qy 241 CTGTGGGGCGCAGCGCGGCTCCAGTGGATTGCGGGCAGACGCGCCAGGACCGCGCT 300  
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Qy 301 TCCACGCTGCGAGGAGACTGGGGAACCGGGGACCCGCTGCTGCGCCCTTCACTTCCAGCT 360  
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Qy 361 CCGCTCTCTCGCGCGAGACCCCGCGCTCCGACCCCTCCCGGGTCCCGGGCCAGGCC 420  
Db 13360 CCGCTCTCTCGCGCGAGACCCCGCGCTCCGACCCCTCCCGGGTCCCGGGCCAGGCC 13419

Qy 421 CTTCCGGGGCCCTCCAGCCCTCCCTCTTTCGCGCGCCCGCGCTCTCTCTCGCGCG 480  
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Qy 481 CGAGTTTCAGGACAGCGCTGCTGCTGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
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Qy	601	GCGAGGTGCTGCGCTGGGCGACGCTTGCTGCGCGCTGGGGGCCACAGAGCTGGCGGCTGG	660
Db	13600	GCGAGGTGCTGCGCTGGGCGACGCTTGCTGCGCGCTGGGGGCCACAGAGCTGGCGGCTGG	13659
Qy	661	TGACGCGCGGGGACCCGGCGGGCTTTCCGCGCGCTGGTGGCCCAGTGCTCTGTGTGCGTGC	720
Db	13660	TGACGCGCGGGGACCCGGCGGGCTTTCCGCGCGCTGGTGGCCCAGTGCTCTGTGTGCGTGC	13719
Qy	721	CTGTGGAGCGACAGCGCGCGCCCGCGCGCCCTTCCTTCGCGCAGGTGSGCCCTCCCGGSG	780
Db	13720	CTGTGGAGCGACAGCGCGCGCCCGCGCGCCCTTCCTTCGCGCAGGTGSGCCCTCCCGGSG	13779
Qy	781	TCGGCGTCCGGCTGGGGTTGAGGCGCGCGGGGGAAACAGCGACATGCGGAGAGCAGCG	840
Db	13780	TCGGCGTCCGGCTGGGGTTGAGGCGCGCGGGGGAAACAGCGACATGCGGAGAGCAGCG	13839
Qy	841	CAGCGACTCAGGGCGCTTCCCGCAGGTGTCCTGCTGAGGAGAGCTGGTGGCCCGAGT	900
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Qy	901	GCTTCGAGAGGCTGTGCGAGCGCGCGCGAGAACGTGCTTGGGCTTTGGGCTTCGCGCTGCT	960
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VERSION     AR490112.1 GI:47257268
KEYWORDS    .
SOURCE      Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 15418)
AUTHORS    Schiff,J.M.
TITLE       Glycosyltransferase vectors for treating cancer
JOURNAL    Patent: US 6713055-A 1 30-MAR-2004;
            Geron Corporation, Menlo Park, CA
            Location/Qualifiers
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VERSION	AR576878.1 GI:56579198
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SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 15418)
AUTHORS	Morin,G.B.; Lichtsteiner,S.P., Vasserot,A.P., Adams,R.R. and Andrews,W.H.
TITLE	Telomerase promoter driving expression of therapeutic gene sequences
JOURNAL	Patent: US 6777203-A 1 17-AUG-2004;
FEATURES	Geron Corporation; Menlo Park, CA
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Best Local Similarity	100.0%;	Pred. No. 3.8e-98;	
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Qy	61	CACGACCTGTTCCAGGGCTCCACATCATGAGCCCTCCCTCGGGTTACCCACAGCT	120
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Db	13540	CCGCGATGCGCGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCGAGCACTACC	13599
Qy	601	GCAGGTGCTGCGCTGGGCCAGTTGCTGGGGCCCTGGGGCCCCCAGGGCTGGGGCTGG	660
Qy	661	TGCAGCGGGGACCCCGCGGCTTTCGCGCGCTGGTGGGCCAGTGCCTGCTGCTGC	720
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Qy	781	TCCGCGTCCGCTGGGGTTGAGGGCGCGCGGGGGAACAGCGACATGCGGAGAGAGCG	840
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VERSION	AX453025.1	GI:21712594	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1	Gold, J. D. and Leebrowski, J. S.	
AUTHORS	Differentiated cells suitable for human therapy		
TITLE	Patent: WO 0242445-A 1 30-MAY-2002;		
JOURNAL	Geront Corporation (US)		
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		Best Local Similarity 100.0%; Pred. No. 3.8e-98;	
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Qy	1	CGTCCGACCTGGAGGACGCCCTGGGTCTCCGATCAGGCCAGCGCCAAAGGTCGCCG	60
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Qy	181	GAGCGGCGCGGGGGAAGCGGGCCAGACCCCGGGTCCGCCGAGCAGCTGCG	240
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Qy	241	CTGTCCGGGCGAGGCGCGGCTCCAGTGGATTCCGGGGCACAGACGCCAGCGCGCT	300
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Qy	781	TCCGCGTCCGCTGGGGTTGAGGGCGCGCGGGGGAACAGCGACATGCGGAGAGAGCG	840
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Qy	841	CAGCGACTCAGGGCGCTTCCCGCGAGGTGCTCTGCTGAAGAGTGTGTGGGCCGAGT	900
Db	13840	CAGCGACTCAGGGCGCTTCCCGCGAGGTGCTCTGCTGAAGAGTGTGTGGGCCGAGT	13899
Qy	901	GCTCAGAGGCTGTGCGAGCGCGCGGAAGACGTGCTGCGCTTCCGCTTCCGCTGCT	960
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Db	24077	GAGCGCGCGCGGGGAGCGCGCCAGACCCCGGGTTCGCCGAGCAGCTGCG	24136
Qy	241	CTGTCGGGGCCAGGCGCGGCTCCAGTGGATTGCGGGGACAGAGCCCAAGGACCGCGCT	300
Db	24137	CTGTCGGGGCCAGGCGCGGCTCCAGTGGATTGCGGGGACAGAGCCCAAGGACCGCGCT	24196
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Qy	361	CCGCTCTCTCGCGCGACCCCGCTCGTCCGACCCCTCCCGGTCCCGGCCAGCC	420
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Db	24377	CGAGTTTCAGGCGCGCTCGCTGCGCGACGTCGGGAGCCCTGGCCCGGCCACCC	24436
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Hominoidea; Homo.

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AUTHORS  
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AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 161252)  
DOE Joint Genome Institute.  
Sequencing of Human Chromosome 5  
Unpublished  
2 (bases 1 to 161252)  
DOE Joint Genome Institute.  
Direct Submission  
Submitted (14-MAR-2002) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
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Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>  
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Center clone name: RPCI-11\_117B23  
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Consensus quality: 158826 bases at least Q20  
Estimated insert size: 175000; agarose-fp estimation  
Estimated insert size: 160452; sum-of-contigs estimation  
Quality coverage: 7.26 in Q20 bases; agarose-fp estimation  
Quality coverage: 7.92 in Q20 bases; sum-of-contigs estimation.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 9 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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Hominidae; Homo.  
REFERENCE 1  
Takakura,M., Kyo,S., Kanaya,T., Hirano,H., Takeda,J., Yutsudo,M.  
and Inoue,M.  
TITLE Cloning of human telomerase catalytic subunit (hTERT) gene promoter  
and identification of proximal core promoter sequences essential

for transcriptional activation in immortalized and cancer cells  
Cancer Res. 59 (3), 551-557 (1999)  
9973199  
2 (bases 1 to 5491)  
Takakura,M., Kyo,S., Kanaya,T., Takeda,J. and Inoue,M.  
Direct Submission  
Submitted (04-AUG-1998) Masahiro Takakura, Kanazawa University,  
School of Medicine, Department of Obstetrics and Gynecology; 13-1,  
Takaramachi, Kanazawa, Ishikawa 920-0934, Japan  
(E-mail:takakura@med.kanazawa-u.ac.jp, Tel:81-76-265-2425,  
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REFERENCE 1. (bases 1 to 26414)  
AUTHORS Wick, M., Zubov, D. and Hagen, G.  
TITLE Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT)

JOURNAL Gene 232 (1), 97-106 (1999)  
PUBMED 10333526  
REFERENCE 2 (bases 1 to 26414)  
AUTHORS Wick, M., Zubov, D. and Hagen, G.  
TITLE Direct Submission  
JOURNAL Submitted (16-FEB-1999) Dept. of Mol. Biol., Bayer AG Leverkusen,  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

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- 9: /cgm2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1001	100.0	4321	3	US-09-402-181B-6
2	1001	100.0	15418	3	US-09-783-203-1
3	1001	100.0	15418	3	US-09-994-427A-1
4	1001	100.0	15418	3	US-09-244-438-1
5	1001	100.0	15418	3	US-09-995-419A-1
6	999.4	99.8	44952	3	US-09-949-016-12197
7	999.4	99.8	44960	3	US-09-949-016-17583
8	999.4	99.8	51552	3	US-09-733-294A-30
9	945.8	94.5	4335	3	US-08-974-549A-6
10	945.8	94.5	4335	3	US-09-721-456-6
11	926.8	92.6	4200	3	US-08-912-951-6
12	502.2	50.2	35871	3	US-09-956-335-2
13	502.2	50.2	35978	3	US-09-956-335-1
14	499	49.9	1677	3	US-09-956-335-3
15	456	45.6	2135	3	US-09-502-498C-51
16	456	45.6	2135	3	US-09-502-424C-51
17	456	45.6	2145	3	US-09-502-498C-55
18	456	45.6	2145	3	US-09-502-424C-55
19	456	45.6	2645	3	US-09-502-498C-59
20	456	45.6	2645	3	US-09-502-424C-59
21	456	45.6	3137	3	US-09-502-498C-79
22	456	45.6	3137	3	US-09-502-424C-79
23	456	45.6	3173	3	US-09-502-498C-67
24	456	45.6	3173	3	US-09-502-424C-67

Sequence 83, Appl  
Sequence 83, Appl  
Sequence 71, Appl  
Sequence 71, Appl  
Sequence 63, Appl  
Sequence 63, Appl  
Sequence 75, Appl  
Sequence 75, Appl  
Sequence 8, Appl  
Sequence 8, Appl  
Sequence 17, Appl  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 224, App  
Sequence 1, Appl  
Sequence 224, App  
Sequence 224, App  
Sequence 3, Appl  
Sequence 1, Appl  
Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-09-402-181B-6  
; Sequence 6, Application US/09402181B  
; Patent NO. 6610839  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Hayley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 633  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/402.181B  
; FILING DATE: 29-Sep-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997

Is an WI

Db	2478	CCGCGATGCGCGCGGCTTCCCGCTGCGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACC	2537
Qy	601	GCAGAGTGCTGCGCGCTGGGCACAGCTTCGTGCGGCGCCTTGGGGCCCCCAGAGGCTTGGCGGCTGG	660
Db	2538	GCAGAGTGCTGCGCGCTGGGCACGTTGTCGGCGCCTTGGGGCCCCCAGAGGCTTGGCGGCTGG	2597
Qy	661	TGCAGCGCGGGAGACCCGCGGCGCTTTTCGCGCGCTGTGTGGCCCAAGTGCTGTGTGTGCGTGC	720
Db	2598	TGCAGCGCGGGAGACCCGCGGCGCTTTTCGCGCGCTGTGTGGCCCAAGTGCTGTGTGTGCGTGC	2657
Qy	721	CTGTGGAGCGACAGCGCGCGCCCCCGCGCGCCCTCTTCGCGCAGGTGGGCGCTCCCGGGG	780
Db	2658	CTGTGGAGCGACAGCGCGCGCCCCCGCGCGCCCTCTTCGCGCAGGTGGGCGCTCCCGGGG	2717
Qy	781	TCCGCGCTCCGCGCTGGGGTTGAGGCGCGCCCGGGGGGAACAGACGACATGCGGAGAGCAGCG	840
Db	2718	TCCGCGCTCCGCGCTGGGGTTGAGGCGCGCCCGGGGGGAACAGACGACATGCGGAGAGCAGCG	2777
Qy	841	CAGGCGACTCAGGGCGCTTCCCCCGCAGGTGTCTCTGCTGAAGAGAGTGTGTGGCCCGAGT	900
Db	2778	CAGGCGACTCAGGGCGCTTCCCCCGCAGGTGTCTCTGCTGAAGAGAGTGTGTGGCCCGAGT	2837
Qy	901	GCTGCGAGAGGCTGTGCGAGCGCGCGCGGCGAAGACGTGTGGCCTTCGGCTTCGGGCTGCT	960
Db	2838	GCTGCGAGAGGCTGTGCGAGCGCGCGCGGCGAAGACGTGTGGCCTTCGGCTTCGGGCTGCT	2897
Qy	961	GGACGGGGCCGCGGGGGCCCCCCCCGAGGCGCTTCAACCACCA	1001
Db	2898	GGACGGGGCCGCGGGGGCCCCCCCCGAGGCGCTTCAACCACCA	2938
RESULT 2			
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; Sequence 1, Application US/09783203			
; Patent No. 6576464			
; GENERAL INFORMATION:			
; APPLICANT: Geron Corporation			
; APPLICANT: Gold, Joseph			
; APPLICANT: Lebkowski, Jane			
; TITLE OF INVENTION: Tpacked stem cells			
; FILE REFERENCE: 096/003			
; CURRENT APPLICATION NUMBER: US/09/783,203			
; CURRENT FILING DATE: 2001-02-13			
; PRIOR APPLICATION NUMBER: 60/253,443			
; PRIOR FILING DATE: 2000-11-27			
; PRIOR APPLICATION NUMBER: 60/253,357			
; PRIOR FILING DATE: 2000-11-27			
; NUMBER OF SEQ ID NOS: 7			
; SOFTWARE: Patent in version 3.0			
; SEQ ID NO 1			
; LENGTH: 15418			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-783-203-1			
Query Match 100.0%; Score 1001; DB 3; Length 15418;			
Best Local Similarity 100.0%; Pred. No. 3.1e-154;			
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CGTCCGAGCTGGAGCAGCCCTGGGTCTCCGATCAGGCCAGCGGCCAAAGGTCGCCG	60
Db	13000	CGTCCGAGCTGGAGCAGCCCTGGGTCTCCGATCAGGCCAGCGGCCAAAGGTCGCCG	1305
Qy	61	CAGGCACCTGTTCCCGAGGGCCTCACATCATGCGCCCTCCCTGGGTATACCCACACAGCCT	120
Db	13060	CAGGCACCTGTTCCCGAGGGCCTCACATCATGCGCCCTCCCTGGGTATACCCACACAGCCT	1311
Qy	121	AGGCGATTGCACTCTCTCCGCTGGGGCCCTCGCTGGGCGCTCCCTGCACTCTGGAGCGC	180
Db	13120	AGGCGATTGCACTCTCTCCGCTGGGGCCCTCGCTGGGCGCTCCCTGCACTCTGGAGCGC	1317
Qy	181	GAGCGCGCGCGCGCGGGGAAGCGCGGCCACACCCCGGGTTCGGCCGAGCAGCTGCG	240



Db 13180 GAGCGCGCGCGCGGGAAGCGCGCCAGACCCCGCGGTCCGCCCGGAGCAGCTGCG 13239  
Qy 241 CTGTCCGGGGCCAGGCGCGGGCTCCAGTGGATTGCGGGGCAAGAGCGCCAGAGACCGGCT 300  
Db 13240 CTGTCCGGGGCCAGGCGCGGGCTCCAGTGGATTGCGGGGCAAGAGCGCCAGAGACCGGCT 13299  
Qy 301 TCCACATGCGGAGGAGCTGGGGAACCCGGGACCCCGTCTGTCGCCCTTCACTTCCAGCT 360  
Db 13300 TCCACATGCGGAGGAGCTGGGGAACCCGGGACCCCGTCTGTCGCCCTTCACTTCCAGCT 13359  
Qy 361 CCGGCTCTCTCGCGCGGAGACCCCGGCGCGTCCGACCCCTCCGGGTCCCGGCGGCGAGCCC 420  
Db 13360 CCGGCTCTCTCGCGCGGAGACCCCGGCGCGTCCGACCCCTCCGGGTCCCGGCGGCGAGCCC 13419  
Qy 421 CCTCGGGGCTCTCCAGCCCTCCCTCTCTTTTCCGGGCGCCCGCCCTCTCTCGCGGCG 480  
Db 13420 CCTCGGGGCTCTCCAGCCCTCCCTCTCTTTTCCGGGCGCCCGCCCTCTCTCGCGGCG 13479  
Qy 481 CGAGTTTCAGGACGCTGCGTCTCTGCGCACAGTGGGAAGCCCTGGCCCCCGGCCACCC 540  
Db 13480 CGAGTTTCAGGACGCTGCGTCTCTGCGCACAGTGGGAAGCCCTGGCCCCCGGCCACCC 13539  
Qy 541 CCGGATGCGCGCGCTCCCGCTGCGAGCGCTGCGTCTGCTGCGGAGCGACTACC 600  
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Db 13660 TGACAGCGCGGGAACCCCGCGGCTTTTCCGCGCGCTGGTGGGCCAGTGCTGCTGCGTGC 13719  
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Qy 781 TCGGCGTCCGCTGGGGTTGAGGGCGCGCGGGGGAACAGCGACATGCGGAGAGCG 840  
Db 13780 TCGGCGTCCGCTGGGGTTGAGGGCGCGCGGGGGAACAGCGACATGCGGAGAGCG 13839  
Qy 841 CAGCGACTCAGGGCGCTTCCCGCGAGGTGCTCTGCTGAAGGAGCTGGTGGCCCGAGT 900  
Db 13840 CAGCGACTCAGGGCGCTTCCCGCGAGGTGCTCTGCTGAAGGAGCTGGTGGCCCGAGT 13899  
Qy 901 GCTCAGAGGCTGTGCGAGCGCGCGGAAGAACTGCTGGCTTCCGCTTCCGCTGCT 960  
Db 13900 GCTCAGAGGCTGTGCGAGCGCGCGGAAGAACTGCTGGCTTCCGCTTCCGCTGCT 13959  
Qy 961 GGACGGGCGCGCGGGGCGCGCGGAGGCTTCCACCA 1001  
Db 13960 GGACGGGCGCGCGGGGCGCGCGGAGGCTTCCACCA 14000

RESULT 3

US-09-994-427A-1  
; Sequence 1, Application US/09994427A  
; Patent No. 6713055  
; GENERAL INFORMATION:  
; APPLICANT: Geron Corporation  
; APPLICANT: Schiff, J. Michael  
; TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER  
; FILE REFERENCE: 083,002  
; CURRENT APPLICATION NUMBER: US/09/994,427A  
; CURRENT FILING DATE: 2002-02-26  
; PRIOR APPLICATION NUMBER: 60/253,395  
; PRIOR FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1  
; LENGTH: 15418  
; TYPE: DNA

; ORGANISM: Homo sapiens  
US-09-994-427A-1  
Query Match 100.0%; Score 1001; DB 3; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 3.1e-154; Indels 0; Gaps 0;  
Matches 1001; Conservative 0; Mismatches 0;  
Qy 1 CGTCCGAGCTGAGGCGAGCCCTGGGTCTCCGATCAGGCGAGCGGCAAGGCTGCGCG 60  
Db 13000 CGTCCGAGCTGAGGCGAGCCCTGGGTCTCCGATCAGGCGAGCGGCAAGGCTGCGCG 13059  
Qy 61 CAGGACCTGTTCCAGGGCTTCAATCATATGGCCCTCTCTGGGTTACCCACAGCT 120  
Db 13060 CAGGACCTGTTCCAGGGCTTCAATCATATGGCCCTCTCTGGGTTACCCACAGCT 13119  
Qy 121 AGGCGGATTGACCTCTCTCGCTGGGGCCCTCGTGGCGTCCCTGACACCTGGAGCGC 180  
Db 13120 AGGCGGATTGACCTCTCTCGCTGGGGCCCTCGTGGCGTCCCTGACACCTGGAGCGC 13179  
Qy 181 GAGCGCGCGCGGCGGGAAGCGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTGCG 240  
Db 13180 GAGCGCGCGCGGCGGGAAGCGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTGCG 13239  
Qy 241 CTGTGCGGGCCAGGCGCGGCTTCCAGTGGATTGCGGGGCAAGAGCGCCAGAGACCGGCT 300  
Db 13240 CTGTGCGGGCCAGGCGCGGCTTCCAGTGGATTGCGGGGCAAGAGCGCCAGAGACCGGCT 13299  
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Qy 361 CCGGCTCTCTCGCGCGGAGACCCCGCGGCTCCGACCCCTCCCGGGTCCCGGCGGCGAGCCC 420  
Db 13360 CCGGCTCTCTCGCGCGGAGACCCCGCGGCTCCGACCCCTCCCGGGTCCCGGCGGCGAGCCC 13419  
Qy 421 CTCTCGGGCTCTCCAGCCCTTCCCTTCTTTCGCGGCGCCCGCCCTCTCTCGCGGCG 480  
Db 13420 CTCTCGGGCTCTCCAGCCCTTCCCTTCTTTCGCGGCGCCCGCCCTCTCTCGCGGCG 13479  
Qy 481 CGAGTTTCAGGACGCTGCGTCTCTGCGCACAGTGGGAAGCCCTGGCCCCCGGCCACCC 540  
Db 13480 CGAGTTTCAGGACGCTGCGTCTCTGCGCACAGTGGGAAGCCCTGGCCCCCGGCCACCC 13539  
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Db 13720 CTGGGAGCGACGCGCGCGCCCGCGCGCTCTCTTCCGCGAGGTGGGCTTCCCGGGG 13779  
Qy 781 TCGGCGTCCGCTGGGGTTGAGGGCGCGCGGGGGAACAGCGACATGCGGAGAGCG 840  
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RESULT 4
US-09-244-438-1
; Sequence 1, Application US/09244438
; Patent No. 6777203
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/09/244,438
; CURRENT FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-09-244-438-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 3.1e-154;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCGGATCAGGCAGCGGCAAGGGTGC CGG 60
Db 13000 CGTCCGACCTGGAGGAGCCCTGGGTCTCGGATCAGGCAGCGGCAAGGGTGC CGG 13059
Qy 61 CAGCACCTGTTCACAGGGCTCCACATCATGTGGCCCTCCTCGGGTTACCCACAGCCT 120
Db 13060 CAGCACCTGTTCACAGGGCTCCACATCATGTGGCCCTCCTCGGGTTACCCACAGCCT 13119
Qy 121 AGGCCGATTCCAGCTCTCTCCGTGGGGCCCTCGCTGGCGTCCCTGCACCCCTGGAGCGC 180
Db 13120 AGGCCGATTCCAGCTCTCTCCGTGGGGCCCTCGCTGGCGTCCCTGCACCCCTGGAGCGC 13179
Qy 181 GAGCGCGCGCGCGGGAGCGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTGCG 240
Db 13180 GAGCGCGCGCGCGGGAGCGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTGCG 13239
Qy 241 CTGTCCGGGGCCAGGCGCGGCTCCAGTGGATTGCGGGGCACAGACGCCCAGGACCGCGCT 300
Db 13240 CTGTCCGGGGCCAGGCGCGGCTCCAGTGGATTGCGGGGCACAGACGCCCAGGACCGCGCT 13299
Qy 301 TCCACCTGCGGAGGACTGGGACCCCGGACCCCGTCTCGTCCCTTCCAGCT 360
Db 13300 TCCACCTGCGGAGGACTGGGACCCCGGACCCCGTCTCGTCCCTTCCAGCT 13359
Qy 361 CCGCCTCTCTCGCGGACCCCGGACCCCGTCCGACCCCTCCCGGTCCCGGCGCAGCC 420
Db 13360 CCGCCTCTCTCGCGGACCCCGGACCCCGTCCGACCCCTCCCGGTCCCGGCGCAGCC 13419
Qy 421 CTTCCGGGGCTCCAGCCCTCCCTCTCTTTCCGGGGCCCGCCCTCTCTCGGGCG 480
Db 13420 CTTCCGGGGCTCCAGCCCTCCCTCTCTTTCCGGGGCCCGCCCTCTCTCGGGCG 13479
Qy 481 CGAGTTTCAGGACGCTCGGTCTCTGTGGCGAGTGGGAAGCCCTGGCCCGGCGCACCC 540
Db 13480 CGAGTTTCAGGACGCTCGGTCTCTGTGGCGAGTGGGAAGCCCTGGCCCGGCGCACCC 13539
Qy 541 CCGGATGCGCGGCTCCCGCTGCGAGCGCTGCGCTCTCTGCTGCGGACCACTACC 600
Db 13540 CCGGATGCGCGGCTCCCGCTGCGAGCGCTGCGCTCTCTGCTGCGGACCACTACC 13599
Qy 601 GCGAGGTGCTCGCCTGGCCACAGTTCTGTGGGCGCTGGGGCCCCAGAGGCTGGCGGTGG 660
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Db 13840 CAGGCGACTCAGGGCGCTTCCCGCGCAGGTGTCTGCTGCTGAAAGAGTGTGTGGCGCGAGT 13899
Qy 901 GCTGCGAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCCGCTTCCGCGCTGCT 960
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Db 13960 GGAAGCGGGCGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14000

RESULT 5
US-09-995-419A-1
; Sequence 1, Application US/09995419A
; Patent No. 6921665
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: McWhir, Jim
; APPLICANT: Gold, Joseph D.
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: 096,004 - SeqList
; FILE REFERENCE: 096,004 - SeqList
; CURRENT APPLICATION NUMBER: US/09/995,419A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-995-419A-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 3.1e-154;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCGGATCAGGCAGCGGCAAGGGTGC CGG 60
Db 13000 CGTCCGACCTGGAGGAGCCCTGGGTCTCGGATCAGGCAGCGGCAAGGGTGC CGG 13059
Qy 61 CAGCACCTGTTCACAGGGCTCCACATCATGTGGCCCTCCTCGGGTTACCCACAGCCT 120
Db 13060 CAGCACCTGTTCACAGGGCTCCACATCATGTGGCCCTCCTCGGGTTACCCACAGCCT 13119
Qy 121 AGGCCGATTCCAGCTCTCTCCGTGGGGCCCTCGCTGGCGTCCCTGCACCCCTGGAGCGC 180
Db 13120 AGGCCGATTCCAGCTCTCTCCGTGGGGCCCTCGCTGGCGTCCCTGCACCCCTGGAGCGC 13179
Qy 181 GAGCGCGCGCGGGAGCGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTGCG 240
Db 13180 GAGCGCGCGCGGGAGCGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTGCG 13239
Qy 241 CTGTCCGGGGCCAGGCGCGGCTCCAGTGGATTGCGGGGCACAGACGCCCAGGACCGCGCT 300
Db 13240 CTGTCCGGGGCCAGGCGCGGCTCCAGTGGATTGCGGGGCACAGACGCCCAGGACCGCGCT 13299
Qy 301 TCCACCTGCGGAGGACTGGGACCCCGGACCCCGTCTCGTCCCTTCCAGCT 360
Db 13300 TCCACCTGCGGAGGACTGGGACCCCGGACCCCGTCTCGTCCCTTCCAGCT 13359
Qy 361 CCGCCTCTCTCGCGGACCCCGGACCCCGTCCGACCCCTCCCGGTCCCGGCGCAGCC 420
Db 13360 CCGCCTCTCTCGCGGACCCCGGACCCCGTCCGACCCCTCCCGGTCCCGGCGCAGCC 13419
Qy 421 CTTCCGGGGCTCCAGCCCTCCCTCTCTTTCCGGGGCCCGCCCTCTCTCGGGCG 480
Db 13420 CTTCCGGGGCTCCAGCCCTCCCTCTCTTTCCGGGGCCCGCCCTCTCTCGGGCG 13479
Qy 481 CGAGTTTCAGGACGCTCGGTCTCTGTGGCGAGTGGGAAGCCCTGGCCCGGCGCACCC 540
Db 13480 CGAGTTTCAGGACGCTCGGTCTCTGTGGCGAGTGGGAAGCCCTGGCCCGGCGCACCC 13539
Qy 541 CCGGATGCGCGGCTCCCGCTGCGAGCGCTGCGCTCTCTGCTGCGGACCACTACC 600
Db 13540 CCGGATGCGCGGCTCCCGCTGCGAGCGCTGCGCTCTCTGCTGCGGACCACTACC 13599
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Db 13240 CTGTGGGGCCAGGCGCGGCTCCAGTGGATTGCGGGGACACAGACGCCAGGACCGGGCT 13299
Qy 301 TCCACAGTGGGGAGGAGTGGGAGACCGGGACACCGCTGCTGCGCCCTTCACTTCCAGCT 360
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Db 13360 CCGCTCTCTCCGCGGAGACCGCGCCGCTGCTCCGACCCCTCCCGGGTCCCGCGCCAGGCC 13419
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Db 13420 CCTCGGGCCCTCCAGCCCTTCCCTTCTTCCGCGGCCCGCGCTCTCTCGCGGG 13479
Qy 481 CGAGTTTCAGGACGAGCGCTGCTGCTGCGACAGTGGGAGCCCTGCGCCCGGACCC 540
Db 13480 CGAGTTTCAGGACGAGCGCTGCTGCTGCGACAGTGGGAGCCCTGCGCCCGGACCC 13539
Qy 541 CCGGATGCCCGCGGCTCCCGCTGCGGAGCGGCTGCTGCTGCGGACGACCTACC 600
Db 13540 CCGGATGCCCGCGGCTCCCGCTGCGGAGCGGCTGCTGCTGCGGACGACCTACC 13599
Qy 601 GCGAGGTGCTCCGCTGGGACAGTTGCTGCGGGCGCTGGGGCCCGAGGCTGGCGGTGG 660
Db 13600 GCGAGGTGCTCCGCTGGGACAGTTGCTGCGGGCGCTGGGGCCCGAGGCTGGCGGTGG 13659
Qy 661 TGCAGCGGGGAGCCCGGGCTTTCGCGCGCTGCTGGGCGGCTGCTGGGCTGGCGTGC 720
Db 13660 TGCAGCGGGGAGCCCGGGCTTTCGCGCGCTGCTGGGCGGCTGCTGGGCTGGCGTGC 13719
Qy 721 CCTGGGACGACGCGCGCCCGCTTCTCCGCGAGTGGGCTTCCCGCGGCTTCCCGGGG 780
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Qy 781 TCGCGCTCCGCTGGGTTGAGGGCGCGCGGGGGAACACGACATCGGAGAGCAGCG 840
Db 13780 TCGCGCTCCGCTGGGTTGAGGGCGCGCGGGGGAACACGACATCGGAGAGCAGCG 13839
Qy 841 CAGGGACTCAGGGGCTTCCCGCGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 13840 CAGGGACTCAGGGGCTTCCCGCGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 13899
Qy 901 GCTGAGAGGCTGTGCGAGCGCGCGCGGGAAGAAAGTGTGCTGCTGCTGCTGCTGCTGCT 960
Db 13900 GCTGAGAGGCTGTGCGAGCGCGCGCGGGAAGAAAGTGTGCTGCTGCTGCTGCTGCTGCT 13959
Qy 961 GGAGCGGCGCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1001
Db 13960 GGAGCGGCGCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14000
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## RESULT 6

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US-09-949-016-12197
; Sequence 12197; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12197
; LENGTH: 44952
; TYPE: DNA
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; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(44952)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12197

Query Match          99.8%; Score 999.4; DB 3; Length 44952;
Best Local Similarity 99.9%; Pred. No. 5.3e-154;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTCCGAGCTGTGAGGAGAGGCTTGGGTCCTCGGATCAGGCGCAGCGGCAAAAGGGTCCGCG 60
Db 1511 CGTCCGAGCTGTGAGGAGAGGCTTGGGTCCTCGGATCAGGCGCAGCGGCAAAAGGGTCCGCG 1570
Qy 61 CAGCACCTGTTCCTCCAGGGCTCCACATCATATGGGCCCTCCCTCGGTTTACCCCAAGCT 120
Db 1571 CAGCACCTGTTCCTCCAGGGCTCCACATCATATGGGCCCTCCCTCGGTTTACCCCAAGCT 1630
Qy 121 AGGCCGATTTCGACCTCTCTCGCTGGGGCCCTCGCTGCGCTCCCTGCAACCTTGGAGCGC 180
Db 1631 AGGCCGATTTCGACCTCTCTCGCTGGGGCCCTCGCTGCGCTCCCTGCAACCTTGGAGCGC 1690
Qy 181 GAGCGCGCGCGCGCGGGAAGCGCGCCAGAACCCCGGGTCCCGCGGAGCAGCTGCG 240
Db 1691 GAGCGCGCGCGCGCGGGAAGCGCGCCAGAACCCCGGGTCCCGCGGAGCAGCTGCG 1750
Qy 241 CTGTCCGGGCGCAGCGCGGCTCCAGTGGATTTCGGGGGACAGACGCCAGGACCGCGCT 300
Db 1751 CTGTCCGGGCGCAGCGCGGCTCCAGTGGATTTCGGGGGACAGACGCCAGGACCGCGCT 1810
Qy 301 TCCACAGTGGCGGAGGAGTGGGGACCGGGGACCCGCTGCTGCGCCCTTCACTTCCAGCT 360
Db 1811 CCCCAGTGGCGGAGGAGTGGGGACCGGGGACCCGCTGCTGCGCCCTTCACTTCCAGCT 1870
Qy 361 CCGCTCTCTCGCGCGAGACCCCGCCCGTCCCGACCCCTTCCCGGGTCCCGCGCCAGGCC 420
Db 1871 CCGCTCTCTCGCGCGAGACCCCGCCCGTCCCGACCCCTTCCCGGGTCCCGCGCCAGGCC 1930
Qy 421 CCTCGGGCCCTCCAGCGCCCTCCCTTCCGCGGGCCCGCCCTCTCTCGCGGG 480
Db 1931 CCTCGGGCCCTCCAGCGCCCTCCCTTCCGCGGGCCCGCCCTCTCTCGCGGG 1990
Qy 481 CGAGTTTCAGGACGAGCTGCTGCTGCTGCGACAGTGGGAAAGCCCTGCGCCCGGACGCC 540
Db 1991 CGAGTTTCAGGACGAGCTGCTGCTGCTGCGACAGTGGGAAAGCCCTGCGCCCGGACGCC 2050
Qy 541 CCGGATGCCCGCGCTTCCCGCTGCGGAGCGGCTGCTGCTGCTGCTGCGGAGCCTACC 600
Db 2051 CCGGATGCCCGCGCTTCCCGCTGCGGAGCGGCTGCTGCTGCTGCTGCGGAGCCTACC 2110
Qy 601 CCGAGGTGCTGCTGCGGACAGTTCGTGCGGGCGCTGGGGCCCGAGGGCTGGCGGGTGG 660
Db 2111 CCGAGGTGCTGCTGCGGACAGTTCGTGCGGGCGCTGGGGCCCGAGGGCTGGCGGGTGG 2170
Qy 661 TGCAGCGCGGGACCCCGCGGCTTTCGCGCGCTGCTGCGCCAGTGTGCTGCTGCTGCTGCT 720
Db 2171 TGCAGCGCGGGACCCCGCGGCTTTCGCGCGCTGCTGCGCCAGTGTGCTGCTGCTGCTGCT 2230
Qy 721 CTTGGAGGACGACGCGCGCCCGCCCGCTTCTTCCCGCAGGTGGGCTTCCCGGGG 780
Db 2231 CTTGGAGGACGACGCGCGCCCGCCCGCTTCTTCCCGCAGGTGGGCTTCCCGGGG 2290
Qy 781 TCGGGCTCCGGCTGGGGTTGAGGGCGCGCGGGGGGAACAGGACATCGGAGAGCAGCG 840
Db 2291 TCGGGCTCCGGCTGGGGTTGAGGGCGCGCGGGGGGAACAGGACATCGGAGAGCAGCG 2350
Qy 841 CAGGCACTCAGGGCGCTTCCCGCAGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 2351 CAGGCACTCAGGGCGCTTCCCGCAGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2410
Qy 901 GCTGAGAGGCTGTGCGAGCGCGCGCGGGAAGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 960
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Db 2411 GCTGACAGGCTGTGTCGAGCGCGCGGAGAACGTCGTGCGCTTTCGGCTTTCGGCTGCT 2470  
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RESULT 7  
US-09-949-016-17583  
; Sequence 17583, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17583  
; LENGTH: 44960  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(44960)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-17583

Query Match 99.8%; Score 999.4; DB 3; Length 44960;  
Best Local Similarity 99.9%; Pred. No. 5.3e-154;  
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CGTCCGACCTGGAGGAGCCCTCGGCTCCCGATCAGGCGGCGCAAGGGTCCCGG 60  
Db 1511 CGTCCGACCTGGAGGAGCCCTCGGCTCCCGATCAGGCGGCGCAAGGGTCCCGG 1570  
Qy 61 CAGCAGCTGTTCAGGAGCCCTCAGATCATGAGCCCTCCCTCGGGTTACCCACAGCCT 120  
Db 1571 CAGCAGCTGTTCAGGAGCCCTCAGATCATGAGCCCTCCCTCGGGTTACCCACAGCCT 1630  
Qy 121 AGCCGAGTTGACCTCTCTCGCTGGGGCCCTCGCTGGCGTCCCTGCACCTGGGAGGC 180  
Db 1631 AGCCGAGTTGACCTCTCTCGCTGGGGCCCTCGCTGGCGTCCCTGCACCTGGGAGGC 1690  
Qy 181 GAGCGGCGCGCGGCGGAGCGCGCCAGACCCCGGGTCCCGCGGAGCAGCTGCG 240  
Db 1691 GAGCGGCGCGCGGCGGAGCGCGCCAGACCCCGGGTCCCGCGGAGCAGCTGCG 1750  
Qy 241 CTGTCCGGGCGAGCGCGGGCTCCAGTGAGTTCCGGGCGACAGACGCCAGGACCGCGCT 300  
Db 1751 CTGTCCGGGCGAGCGCGGGCTCCAGTGAGTTCCGGGCGACAGACGCCAGGACCGCGCT 1810  
Qy 301 TCCACGTTGGGAGGAGCTGGGAGCCGGGACCCGTCCTCGGAGCCCTCCCGGGTCCCGGCGGAGCC 360  
Db 1811 CCCCAGCTGGGAGGAGCTGGGAGCCGGGACCCGTCCTCGGAGCCCTTTCACCTTCCAGCT 1870  
Qy 361 CCGGCTCTCTCCGCGGAGACCCCGGCTCCCGGAGCCCTCCCGGGTCCCGGCGGAGCC 420  
Db 1871 CCGGCTCTCTCCGCGGAGACCCCGGCTCCCGGAGCCCTCCCGGGTCCCGGCGGAGCC 1930  
Qy 421 CCTCGGGCCCTCCAGCCCTCCCTCTCTTTCGGGGCCCGGCGCTCTCTCGGGGG 480  
Db 1931 CCTCGGGCCCTCCAGCCCTCCCTCTCTTTCGGGGCCCGGCGCTCTCTCGGGGG 1990  
Qy 481 CGAGTTTCAGCAGCGGCTCGCTCTCTGTCGCGCAGCTGGGAGCCCTTGGCCCCGCCACC 540

Db 1991 CGAGTTTCAGCAGCGCTCGCTCTCTGTCGCGAGGAGCCCTTGGCCCCGCCACC 2050  
Qy 541 CCGCGATGCGCGCGCTCCCGCTGCGGAGCCGCTGCGCTCCCTGCTGCGGAGCCACTACC 600  
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RESULT 8  
US-09-733-294A-30  
; Sequence 30, Application US/09733294A  
; Patent No. 6492171  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: William Gaarde  
; APPLICANT: Susan M. Freier  
; APPLICANT: Edward V. Wanciewicz  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION  
; FILE REFERENCE: ISPH-0527  
; CURRENT APPLICATION NUMBER: US/09/733,294A  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: 09/572,423  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 108  
; SEQ ID NO 30  
; LENGTH: 51552  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (1)...(11492)  
; OTHER INFORMATION: exon 1  
; NAME/KEY: intron  
; LOCATION: (11493)...(11596)  
; OTHER INFORMATION: intron 1  
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; LOCATION: (11597)...(12950)  
; OTHER INFORMATION: exon 2  
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; LOCATION: (21567)...(21762)  
; OTHER INFORMATION: exon 3  
; NAME/KEY: intron

; LOCATION: (21763)...(23851)  
; OTHER INFORMATION: intron 3  
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; OTHER INFORMATION: exon 4  
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; LOCATION: (24033)...(24719)  
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; OTHER INFORMATION: exon 8  
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; LOCATION: (31359)...(33843)  
; OTHER INFORMATION: intron 8  
; NAME/KEY: unsure  
; LOCATION: 31450  
; OTHER INFORMATION: unknown  
; NAME/KEY: exon  
; LOCATION: (33844)...(33957)  
; OTHER INFORMATION: exon 9  
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; LOCATION: (38074)...(41874)  
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; LOCATION: (41875)...(42001)  
; OTHER INFORMATION: exon 12  
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; LOCATION: (42002)...(42881)  
; OTHER INFORMATION: intron 12  
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; OTHER INFORMATION: intron 14  
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; OTHER INFORMATION: exon 15  
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; LOCATION: (47710)...(50544)  
; OTHER INFORMATION: exon 16  
US-09-733-294A-30

Query Match 99.8%; Score 999.4; DB 3; Length 51552;  
Best Local Similarity 99.9%; Pred. No. 5.2e-154;  
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CGTCGGACCTGGAGGAGCCCTGGCTCTCGGATCAGGCCAGCGGGCCAAAGGGTGGCGG 60  
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Qy 61 CACGACCTGTTCCAGGGCTCCACATCATATGGCCCTCTCCCTCGGGTTACCCACAGCT 120  
Db 10789 CACGACCTGTTCCAGGGCTCCACATCATATGGCCCTCTCCCTCGGGTTACCCACAGCT 10848  
Qy 121 AGCCGATTTCACCTCTCTCGCTGGGGCCCTCGCTGGCGTCCCTGACACCTTGGAGGCG 180  
Db 10849 AGCCGATTTCACCTCTCTCGCTGGGGCCCTCGCTGGCGTCCCTGACACCTTGGAGGCG 10908  
Qy 181 GAGCGGCGCGGGCGGAGCGCGCCAGACCCCGGGTTCGCCCGGAGCAGCTGG 240  
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Qy 241 CTGTGGGGCCAGGCGGGCTCCACATCATATGGGATTCGCGGACAGAGCCCGGACCGCGT 300  
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Qy 361 CCGCTCTCTCGCGCGGAGCCCGGCGCGTCCGACCCCTCCCGGGTCCCGCCAGGCC 420  
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Qy 421 CCTCGGGCCCTCCAGCCCTCCCTTCTCTTTCGCGGCGCCCGCCCTCTCTCTCGCGG 480  
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Qy 481 CGAGTTTCAGGACGCTGCTCTCTGTCGCGACGCTGGGAGCCCTGGCGCCCGGCGCACCC 540  
Db 11209 CGAGTTTCAGGACGCTGCTCTCTGTCGCGACGCTGGGAGCCCTGGCGCCCGGCGCACCC 11268  
Qy 541 CCGGATGCGCGCGCTCCCGCTCGCGAGCCGCTGCGCTCCCTGCTGCGGACCACTACC 600  
Db 11269 CCGGATGCGCGCGCTCCCGCTCGCGAGCCGCTGCGCTCCCTGCTGCGGACCACTACC 11328  
Qy 601 GCGAGGTGCTGCGCTGGCCACAGTTTCGTCGCGCGCTGGGGCCCGGCGCTGGCGGCTGG 660  
Db 11329 GCGAGGTGCTGCGCTGGCCACAGTTTCGTCGCGCGCTGGGGCCCGGCGCTGGCGGCTGG 11388  
Qy 661 TGCAGCGCGGGAACCCCGCGCTTTCGCGCGCTGGTGGCCAGTGCCTGCTGCTGGCTGC 720  
Db 11389 TGCAGCGCGGGAACCCCGCGCTTTCGCGCGCTGGTGGCCAGTGCCTGCTGCTGGCTGC 11448  
Qy 721 CCTGGAGCGACGGCGCGCCCGCGCTCCCTTCCTCGCGAGGTGGGCTCCCGCGG 780  
Db 11449 CCTGGAGCGACGGCGCGCCCGCGCTCCCTTCCTCGCGAGGTGGGCTCCCGCGG 11508  
Qy 781 TCGCGCTCCGCTGGGGTTGAGGGCGCGCGGGGGAACACAGCAATTCGCGAGACAGG 840  
Db 11509 TCGCGCTCCGCTGGGGTTGAGGGCGCGCGGGGGAACACAGCAATTCGCGAGACAGG 11568  
Qy 841 CAGCGACTCAGGGCGCTTCCCGCGAGTGTCTGCTGTAAGGAGCTGGTGGCCCGAGT 900  
Db 11569 CAGCGACTCAGGGCGCTTCCCGCGAGTGTCTGCTGTAAGGAGCTGGTGGCCCGAGT 11628







537	QY	ACCCCGCGATGCGCGCGCTCCCGCTGCCGAGCCGTGCGTCCCTGCTGCGGAGCCAC	596
2487	Db	ACCCCGCGATGCGCGCGCTCCCGCTGCCGAGCCGTGCGTCCCTGCTGCGCAGCCAC	2546
597	QY	TACCGGAGGTGCTGCCGCTGGCCACCTTCGTGCGGCGCTTGGGGCCCCCAGGGCTGGCGG	656
2547	Db	TACCGGAGGTGCTGCCGCTGGCCACCTTCGTGCGGCGCTTGGGGCCCCCAGGGCTGGCGG	2606
657	QY	CTGCTGCAGCGCGGGGACCCGGCGGCTTTCGGCGCGCTGTGTGCCCCAGTGCCTTGGTGTGC	716
2607	Db	CTGCTGCAGCGCGGGGACCCGGCGGCTTTCGGCGCGCTGTGTGCCCCAGTGCCTTGGTGTGC	2666
717	QY	GTGCGCTTGGAGCGCACGGCGCGCCCCCGCGCCCCCTCTCTTCGCCAGGTGGGGCTCCCC	776
2667	Db	GTGCGCTTGGAGCGCACGGCGCGCCCCCGCGCCCCCTCTCTTCGCCAGGTGGGGCTCCCC	2726
777	QY	GGGGTCGGCGCTCCGGCTTGGGGTTGAGGGCGCGCGGGGGAAACAGCGACATGCGCGAGAGC	836
2727	Db	GGGGTCGGCGCTCCGGCTTGGGGTTGAGGGCGCGCGGGGGAAACAGCGACATGCGCGAGAGC	2786
837	QY	AGCGGAGGCGACTCAGGGCGCTTCCCGCGAGGTGTCTCGCTGGAAGGAGCTGGTGGCCCC	896
2787	Db	AGCGGAGGCGACTCAGGGCGCTTCCCGCGAGGTGTCTCGCTGGAAGGAGCTGGTGGCCCC	2846
897	QY	GAGTGTGCAGAGGCTGTGCAGCGCGCGCGAAGAACGTGTGGCTTCCGGCTTGGCGC	956
2847	Db	GAGTGTGCAGAGGCTGTGCAGCGCGCGCGAAGAACGTGTGGCTTCCGGCTTGGCGC	2906
957	QY	TGCTGGACGGGGCCCCCGGGGGCCCCCCCCCGAGGCTTTCACACCA	1001
2907	Db	TGCTGGACGGGGCCCCCGGGGGCCCCCCCCCGAGGCTTTCACACCA	2951

## RESULT 11

US-08-912-951-6  
; Sequence 6, Application US/08912951  
; Patent No. 6475789  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
; THERAPEUTIC METHODS  
; NUMBER OF SEQUENCES: 335  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,951  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:





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Db 34220 CCTCCGGGCGCTCCAGCCCTCCCTTCTCTTTCGGGGCCCGCCCTCTCCTCGGGCG 34161
Qy 481 CGAGTTTCAGGCGCGCTGGTCTGTC 507
Db 34160 CGAGTTTCAGGCGCGCTGATTATGTC 34134

RESULT 14
US-09-556-335-3/c
; Sequence 3, Application US/09556335
; Patent No. 6627190
; GENERAL INFORMATION:
; APPLICANT: WOLD, William
; APPLICANT: TOTH, Karoly
; APPLICANT: KUPPASWAMI, Mohan
; APPLICANT: DORONIN, Konstantin
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
; TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
; FILE REFERENCE: 16153-8394
; CURRENT APPLICATION NUMBER: US/09/956,335
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1677
; TYPE: DNA
; ORGANISM: Adenovirus
; US-09-556-335-3

Query Match 49.9%; Score 499; DB 3; Length 1677;
Best Local Similarity 100.0%; Pred. No. 9.1e-73; Mismatches 0; Indels 0; Gaps 0;
Matches 499; Conservative 0;

Qy 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCGAGCGGCAAGGCTGCCCG 60
Db 501 CGTCCGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCGAGCGGCAAGGCTGCCCG 442
Qy 61 CAGCACCTGTTCCAGGCGCTCACAATCATATGCGCCCTCCTCGGGTTACCCACAGCCT 120
Db 441 CAGCACCTGTTCCAGGCGCTCACAATCATATGCGCCCTCCTCGGGTTACCCACAGCCT 382
Qy 121 AGGCGGATTCAGCTCTCTCGCTGGGCGCTCTCGCTGGGCTCCCTGACCTGGGAGCGC 180
Db 381 AGGCGGATTCAGCTCTCTCGCTGGGCGCTCTCGCTGGGCTCCCTGACCTGGGAGCGC 322
Qy 181 GAGCGGCGCGGGCGGGGAGCGCGCCAGACCCCGGGTCCGCGGAGCAGCTGCG 240
Db 321 GAGCGGCGCGGGCGGGGAGCGCGCCAGACCCCGGGTCCGCGGAGCAGCTGCG 262
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Db 261 CTGTGGGGCGAGCGCGGGCTCCAGTGGAATTGGGGGCAAGAGCGCCGAGCGCGCT 202
Qy 301 TCCACGTTGGGAGGAGCTGGGAGCCCGGACCCGCTCTGCGCCCTTCACTTCCAGCT 360
Db 201 TCCACGTTGGGAGGAGCTGGGAGCCCGGACCCGCTCTGCGCCCTTCACTTCCAGCT 142
Qy 361 CCGCTCTCTCGCGCGAGCCCGCGCTCCCGACCCCTCCCGGCTCCCGGCGCCAGCCC 420
Db 141 CCGCTCTCTCGCGCGAGCCCGCGCTCCCGACCCCTCCCGGCTCCCGGCGCCAGCCC 82
Qy 421 CCTCGGGCGCTCCAGCGCTCCCTCTCTTTCGGGGCGCCCGCTCTCTCGGGCG 480
Db 81 CCTCGGGCGCTCCAGCGCTCCCTCTCTTTCGGGGCGCCCGCTCTCTCGGGCG 22

Qy 481 CGAGTTTCAGGCGCGCTG 499
Db 21 CGAGTTTCAGGCGCGCTG 3
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RESULT 15
US-09-502-498C-51
; Sequence 51, Application US/09502498C
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; Patent No. 6846662
; GENERAL INFORMATION:
; APPLICANT: Kilian, Andrzej
; APPLICANT: Bowtell, David
; TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 407C2
; CURRENT APPLICATION NUMBER: US/09/502,498C
; CURRENT FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 2135
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1871)..(1873)
; OTHER INFORMATION: Wherein N is A, C, G or T
; FEATURE:
; OTHER INFORMATION: Truncated Telomerase (ver. 2); with
; OTHER INFORMATION: Intron Y
; US-09-502-498C-51

Query Match 45.6%; Score 456; DB 3; Length 2135;
Best Local Similarity 100.0%; Pred. No. 8.5e-66; Mismatches 0; Indels 0; Gaps 0;
Matches 456; Conservative 0;

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Db 1 ATGCGCGCGCTCCCGCTCCCGAGCGGTGCGTCCCTGCTGCGAGCCACTACCGCGAG 60
Qy 606 GTGCTGCGCTGCGCAGCTTCGTGCGCGCGCTGGGGCCCGAGGCTGGCGCTGGTGCAG 665
Db 61 GTGCTGCGCTGCGCAGCTTCGTGCGCGCGCTGGGGCCCGAGGCTGGCGCTGGTGCAG 120
Qy 666 CGCGGGGAGCCCGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGGTGGTGGTGG 725
Db 121 CGCGGGGAGCCCGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGGTGGTGGTGG 180
Qy 726 GAGCGACGCGCGCGCGCGCGCGCTTCCCTTCCGCGAGGTGGGCTTCCCGGGGTGCGC 785
Db 181 GAGCGACGCGCGCGCGCGCGCGCTTCCCTTCCGCGAGGTGGGCTTCCCGGGGTGCGC 240
Qy 786 GTCCGCTGGGGTTGAGGGCGCGCGGGGGAACAGCGACATGCGGAGAGAGCGCAGGC 845
Db 241 GTCCGCTGGGGTTGAGGGCGCGCGGGGGAACAGCGACATGCGGAGAGAGCGCAGGC 300
Qy 846 GACTCAGGGCGCTTCCCGCGAGGTGCTCCTGAAAGGAGCTGGTGGCCCGAGTGTGC 905
Db 301 GACTCAGGGCGCTTCCCGCGAGGTGCTCCTGAAAGGAGCTGGTGGCCCGAGTGTGC 360
Qy 906 AGAGGCTGTGCGAGCGCGCGCGCGAAGAACGTGTGCTTTCGGCTTCGCGTCTGTAAG 965
Db 361 AGAGGCTGTGCGAGCGCGCGCGCGAAGAACGTGTGCTTTCGGCTTCGCGTCTGTAAG 420
Qy 966 GGGCGCGCGGGCGCGCGCGCGCGAGGCTTTCACACCA 1001
Db 421 GGGCGCGCGGGCGCGCGCGCGCGAGGCTTTCACACCA 456

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Job time : 206 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 10:37:31 ; Search time 949.333 Seconds  
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Perfect score: 1001  
Sequence: 1 ggcgggattacagccccc.....gggaccagtggcgtggc 1001

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1001	100.0	4321	6	US-10-325-810-6
2	1001	100.0	15418	3	US-09-783-203-1
3	1001	100.0	15418	3	US-09-994-427A-1
4	1001	100.0	15418	3	US-09-995-419A-1
5	1001	100.0	15418	5	US-10-141-220-1
6	1001	100.0	15418	5	US-10-023-969-1
7	1001	100.0	15418	5	US-10-206-447-1
8	1001	100.0	15418	7	US-10-674-836-1
9	1001	100.0	15418	7	US-10-811-012-1
10	988.6	98.8	4293	8	US-10-456-830-1
11	972.8	97.2	5126	8	US-10-840-455-1
12	972.8	97.2	11276	8	US-10-840-455-3
13	972.8	97.2	26414	8	US-10-840-455-43
14	972.8	97.2	51552	3	US-09-733-294A-30
15	930.8	93.0	4335	8	US-10-877-124-6
16	930.8	93.0	4335	8	US-10-877-022-6
17	930.8	93.0	4335	8	US-10-877-146-6
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19	677.8	67.7	35978	3	US-09-956-335-1
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21	643.2	64.3	4356	7	US-10-240-589C-144
22	636	63.5	4356	7	US-10-240-589C-143
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24	240	24.0	3186778	5	US-10-027-632-174961	Sequence 174961,
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26	229.8	23.0	4200	5	US-10-044-692-6	Sequence 6, Appli
27	229.8	23.0	4200	5	US-10-044-692-6	Sequence 6, Appli
28	136.4	13.6	158980	8	US-10-422-522-32	Sequence 32, Appli
29	134.2	13.4	18596	3	US-09-880-107-1590	Sequence 1590, Ap
30	134.2	13.4	18596	3	US-09-967-768A-119	Sequence 119, App
31	134.2	13.4	18596	3	US-09-954-531-124	Sequence 124, App
32	134.2	13.4	18596	3	US-09-954-531-348	Sequence 348, App
33	134.2	13.4	18596	8	US-10-629-313-140	Sequence 140, App
34	134.2	13.4	18596	9	US-10-843-641A-1191	Sequence 1191, Ap
35	134.2	13.4	18596	9	US-10-843-641A-1415	Sequence 1415, Ap
36	134.2	13.4	18596	9	US-10-843-641A-6264	Sequence 6264, Ap
C 37	133.8	13.3	591	4	US-09-925-065A-822099	Sequence 822099,
C 38	132.8	13.3	584	4	US-09-925-065A-566446	Sequence 566446,
C 39	132.8	13.3	196686	5	US-10-087-192-484	Sequence 484, App
C 40	132.4	13.2	584	4	US-09-925-065A-566447	Sequence 566447,
C 41	132.2	13.2	565	4	US-09-925-065A-740337	Sequence 740337,
C 42	132.2	13.2	567	4	US-09-925-065A-740801	Sequence 740801,
C 43	132.2	13.2	594	4	US-09-925-065A-682612	Sequence 682612,
C 44	132.2	13.2	594	4	US-09-925-065A-682613	Sequence 682613,
C 45	132.2	13.2	24295	7	US-10-317-277A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-10-325-810-6  
; Sequence 6, Application US/10325810  
; Publication No. US20030204069A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 633  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/325,810  
; FILING DATE: 20-Dec-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/402,181  
; FILING DATE: 29-Sep-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951

;; FILING DATE: 14-AUG-1997  
;; APPLICATION NUMBER: US 08/915,503  
;; FILING DATE: 14-AUG-1997  
;; APPLICATION NUMBER: WO PCT/US97/17885  
;; FILING DATE: 01-OCT-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Aussenhus, Scott L.  
;; REGISTRATION NUMBER: 42,271  
;; REFERENCE/DOCKET NUMBER: 015389-002620US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4321 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: -  
;; LOCATION: 1..4321  
;; OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"  
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;; NAME/KEY: intron  
;; LOCATION: 2702..2804  
;; OTHER INFORMATION: /note= "intron 1"  
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;; NAME/KEY: intron  
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;; OTHER INFORMATION: /note= "intron 2"  
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;; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-325-810-6

Query Match 100.0%; Score 1001; DB 6; Length 4321;  
Best Local Similarity 100.0%; Pred. No. 6.9e-295;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGCTGGTCTCGAATCTCTGACCTCAGA 120  
Db 498 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGCTGGTCTCGAATCTCTGACCTCAGA 557

Qy 121 TGATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 180  
Db 558 TGATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 617

Qy 181 GCTCAGAAATTACTCTGTTTAGAAACATCTGGGTCTGAGTAGGAAGCTCACCCCACTCA 240  
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Qy 241 AGTGTCTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTGTTAGAACACTCTTGA 300  
Db 678 AGTGTCTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTGTTAGAACACTCTTGA 737

Qy 301 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGACACC 360  
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Qy 361 ATAATACCTGGGGTCTCTTCTGGGTATCAGGATCTTCATTTGAATGCCGGAGGGTTTCC 420  
Db 798 ATAATACCTGGGGTCTCTTCTGGGTATCAGGATCTTCATTTGAATGCCGGAGGGTTTCC 857

Qy 421 TCGGCATGCACATGCTGTTAACTTACTCCAGATAATCTCTGCTTCCATTTCTCTCTTC 480  
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Qy 481 CCTCTTTTAAATTTGTTTTCTATGTTGGCTTCTCTGCAGAGAACAGGTGTAAGCTACA 540  
Db 918 CCTCTTTTAAATTTGTTTTCTATGTTGGCTTCTCTGCAGAGAACAGGTGTAAGCTACA 977

Qy 541 ACTTAACCTTTTGTGGAACAAAATTTCCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA 600  
Db 978 ACTTAACCTTTTGTGGAACAAAATTTCCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA 1037

Qy 601 TTCACAAACACAGCCCTTTTAAAAAGGCTTAGGGATCACTAAGGGGATTTCTTAGAAGAGCG 660  
Db 1038 TTCACAAACACAGCCCTTTTAAAAAGGCTTAGGGATCACTAAGGGGATTTCTTAGAAGAGCG 1097

Qy 661 ACCCGTAATCCTAAGTATTTTACAAGACGAGGCTTAACCTCCAGCGAGCGTGACGCCAGG 720  
Db 1098 ACCCGTAATCCTAAGTATTTTACAAGACGAGGCTTAACCTCCAGCGAGCGTGACGCCAGG 1157

Qy 721 GAGGGTGCAGGGCTGTTCAAAATGCTAGCTCCATAAATAAGCAATTTCTCCGGCAGTT 780  
Db 1158 GAGGGTGCAGGGCTGTTCAAAATGCTAGCTCCATAAATAAGCAATTTCTCCGGCAGTT 1217

Qy 781 TCTGAAAGTAGGAAAGGTTACATTTTAAGGTTTGGGTTTGTAGCAATTTCACTGTTTGCAGA 840  
Db 1218 TCTGAAAGTAGGAAAGGTTACATTTTAAGGTTTGGGTTTGTAGCAATTTCACTGTTTGCAGA 1277

Qy 841 CCTCAGCTACAGCATCCCTGCAAGGCTTCGGGAGACCCAGAAGTTTCTCGCCCTTAGAT 900  
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Qy 901 CCAAACTTAGGCAACCGGAGTCTGGATTCCTGGGAAGTCTCAGCTGTCTGGGGTTGT 960  
Db 1338 CCAAACTTAGGCAACCGGAGTCTGGATTCCTGGGAAGTCTCAGCTGTCTGGGGTTGT 1397

Qy 961 GCCGGGGCCCCAGGTCTGGAGGGGACCCAGTGGCCGTGTGGC 1001  
Db 1398 GCCGGGGCCCCAGGTCTGGAGGGGACCCAGTGGCCGTGTGGC 1438

## RESULT 2

US-09-783-203-1  
; Sequence 1, Application US/09783203  
; Patent No. US20020098582A1  
; GENERAL INFORMATION:  
; APPLICANT: Geron Corporation  
; APPLICANT: Gold, Joseph  
; APPLICANT: Lebkowski, Jane  
; TITLE OF INVENTION: Tpacked stem cells  
; FILE REFERENCE: 096/003  
; CURRENT APPLICATION NUMBER: US/09/783,203  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: 60/253,443  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/253,357  
; PRIOR FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 15418  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-783-203-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 1.4e-294;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGATTACAGGACCGCCGACCATGCGCAGCTAAATTTTGTATTTTGTATTTAGTAGAGA 60  
Db 11500 GGCTGGGATTACAGGACCGCCGACCATGCGCAGCTAAATTTTGTATTTTGTATTTAGTAGAGA 11559

Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAATCTCTGACCTCAGA 120  
Db 11560 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAATCTCTGACCTCAGA 11619

Qy 121 TGATCCACCTGCTCTGCTCTCTAAAGTGTGCGGATTTACAGGTGTGAGCCACCATGCCCA 180  
Db 11620 TGATCCACCTGCTCTGCTCTCTAAAGTGTGCGGATTTACAGGTGTGAGCCACCATGCCCA 11679



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QY 961 GCGGGGCCCCAGTCTGGAGGGAGCCAGTGGCGGTGGC 1001
Db 12460 GCGGGGCCCCAGTCTGGAGGGAGCCAGTGGCGGTGGC 12500

RESULT 4
US-09-995-419A-1
; Sequence 1, Application US/09995419A
; Publication No. US20030032187A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: McWhir, Jim
; APPLICANT: Gold, Joseph D.
; TITLE OF INVENTION: 096.004 - SeqList
; FILE REFERENCE: 096.004 - SeqList
; CURRENT APPLICATION NUMBER: US/09/995,419A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-995-419A-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 1.4e-294;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CGGGGGTGGGGTGGGGTTCACCATGTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 120
Db 11560 CGGGGGTGGGGTGGGGTTCACCATGTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 11619

QY 121 TGATCCACCTGCCTCTGCCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 180
Db 11620 TGATCCACCTGCCTCTGCCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 11679

QY 181 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCAGCCCACTCA 240
Db 11680 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCAGCCCACTCA 11739

QY 241 AGTGTGTGTGTTTAAAGCCATGATAGAAATTTTATTTATTTGTAGAACACTCTTGA 300
Db 11740 AGTGTGTGTGTTTAAAGCCATGATAGAAATTTTATTTATTTGTAGAACACTCTTGA 11799

QY 301 TGTTTTACCTGTGATCACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
Db 11800 TGTTTTACCTGTGATCACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 11859

QY 361 ATAATACCTGGGGTGTCTTCTGGGTATCAGGCATCTTCATTTGAATGCCGGAGGGCTTTC 420
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QY 421 TCGCCATGCATGGGTGTTTAACTTACTCAGCATATCTTCTGCTTCAATTTCTTCTTTC 480
Db 11920 TCGCCATGCATGGGTGTTTAACTTACTCAGCATATCTTCTGCTTCAATTTCTTCTTTC 11979

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QY 541 ACTTAACTTTTGTGGAAACAAATTTTCAAACCGCCCTTTGGCCCTAGTGGCGAGACAA 600
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QY 601 TTCACAAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAAGGGGATTTCTAGAAGAGCG 660
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Db 12220 GAGGGTGGAGGCGCTGTTCAAATGCTAGCTTCATAAATAAAGCAATTTCTCCGGCAGTT 12279

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QY 901 CCAAACTTGAGCAACCCGAGTCTGGAATCTCGGGAAGTCTCAGCTGTCTCGCGTGT 960
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Db 12460 GCGGGGCCCCAGGCTCTGGAGGGGACCATGTCGCGGTGGC 12500

RESULT 5
US-10-141-220-1
; Sequence 1, Application US/10141220
; Publication No. US20030040111A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tpacked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/10/141,220
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/09/783,203
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-141-220-1

Query Match 100.0%; Score 1001; DB 5; Length 15418;
Best Local Similarity 100.0%; Pred. No. 1.4e-294;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCTGGGATTACAGGCACCCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 60
Db 11500 GGCCTGGGATTACAGGCACCCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 11559

QY 61 CGGGGGTGGGGTGGGGTTCACCATGTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 120
Db 11560 CGGGGGTGGGGTGGGGTTCACCATGTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 11619

QY 121 TGATCCACCTGCCTCTGCCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 180
Db 11620 TGATCCACCTGCCTCTGCCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 11679

QY 181 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCAGCCCACTCA 240
Db 11680 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCAGCCCACTCA 11739

QY 241 AGTGTGTGTGTTTAAAGCCATGATAGAAATTTTATTTATTTGTAGAACACTCTTGA 300
Db 11740 AGTGTGTGTGTTTAAAGCCATGATAGAAATTTTATTTATTTGTAGAACACTCTTGA 11799

QY 301 TGTTTTACCTGTGATCACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
Db 11800 TGTTTTACCTGTGATCACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 11859

QY 361 ATAATACCTGGGGTGTCTTCTGGGTATCAGGCATCTTCATTTGAATGCCGGAGGGCTTTC 420
Db 11860 ATAATACCTGGGGTGTCTTCTGGGTATCAGGCATCTTCATTTGAATGCCGGAGGGCTTTC 11919

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QY 481 CCTCTTTTAAATATGTTTCTTATGTTGGCTTCTGTCAGAGAACAGGTAGGTAGCTACA 540
Db 11980 CCTCTTTTAAATATGTTTCTTATGTTGGCTTCTGTCAGAGAACAGGTAGGTAGCTACA 12039

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Qy 661 ACCGTAATCTTAAGTATTATTAAGAAGAGGCTAAACCTCAGCGAGCGTGACACCCAGG 720
|||||
Db 12160 ACCGTAATCTTAAGTATTATTAAGAAGAGGCTAAACCTCAGCGAGCGTGACACCCAGG 12219
|||||
Qy 721 GAGGTCGAGGCGCTGTTCAAAATGCTAGCTCCATAATAAAGCAATTTCTCCGGCAGTT 780
|||||
Db 12220 GAGGTCGAGGCGCTGTTCAAAATGCTAGCTCCATAATAAAGCAATTTCTCCGGCAGTT 12279
|||||
Qy 781 TCTGAAAGTAGGAAAGGTTACATTTAAGGTTGGGTTTGTAGCATTTTCAGTGTGTGCCGA 840
|||||
Db 12280 TCTGAAAGTAGGAAAGGTTACATTTAAGGTTGGGTTTGTAGCATTTTCAGTGTGTGCCGA 12339
|||||
Qy 841 CCTCAGCTACAGCATCTCTGCAAGGCTCGGAGAGCCAGAAAGTTTCTCGCCCTTAGAT 900
|||||
Db 12340 CCTCAGCTACAGCATCTCTGCAAGGCTCGGAGAGCCAGAAAGTTTCTCGCCCTTAGAT 12399
|||||
Qy 901 CCAAACTTGAGCAACCGGAGTCTGGATTCTCTGGAGTCTCAGCTGTCTCGGGTGT 960
|||||
Db 12400 CCAAACTTGAGCAACCGGAGTCTGGATTCTCTGGAGTCTCAGCTGTCTCGGGTGT 12459
|||||
Qy 961 GCCGGGGCCCCAGGCTCTGAGGGGACCAAGTGGCGGTGTGGC 1001
|||||
Db 12460 GCCGGGGCCCCAGGCTCTGAGGGGACCAAGTGGCGGTGTGGC 12500
|||||

RESULT 8
US-10-674-836-1
; Sequence 1, Application US/10674836
; Publication No. US20040072787A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; TITLE OF INVENTION: Regulatory Sequences and Methods of Using
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/10/674,836
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/244,438
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-10-674-836-1

Query Match 100.0%; Score 1001; DB 7; Length 15418;
Best Local Similarity 100.0%; Pred. No. 1.4e-294; Indels 0; Gaps 0;
Matches 1001; Conservative 0; Mismatches 0;

Qy 1 GGCTGGGATTACAGGACCCGCCACCATGCCCAGCTAAATTTTGTATTTTAGTAGAGA 60
Db 11500 GGCTGGGATTACAGGACCCGCCACCATGCCCAGCTAAATTTTGTATTTTAGTAGAGA 11559
Qy 61 CGGGGGTGGGGTGTACCATGTTGGCAGGCTGCTCGAATCTTGACCTCAGA 120
Db 11560 CGGGGGTGGGGTGTACCATGTTGGCAGGCTGCTCGAATCTTGACCTCAGA 11619
Qy 121 TGATCCACCTGCCTCTGCCTCCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCCA 180
Db 11620 TGATCCACCTGCCTCTGCCTCCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCCA 11679
Qy 181 GCTCAGAAATTACTCTGTTTGTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240
Db 11680 GCTCAGAAATTACTCTGTTTGTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 11739
Qy 241 AGTGTGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTGTAGAACACTCTTGA 300
Db 11740 AGTGTGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTGTAGAACACTCTTGA 11799
Qy 301 TGTTTTACCTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
Db 11800 TGTTTTACCTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 11859
Qy 361 ATAATCTGGGTGCTCTTCTGGGTATCAGCATCTTCAATGAATGCCGGAGGCGTTTCC 420
Db 11860 ATAATCTGGGTGCTCTTCTGGGTATCAGCATCTTCAATGAATGCCGGAGGCGTTTCC 11919
Qy 421 TCGCCATGCACATGGTGTAAATTAATCTCCAGCATATCTTCTGCTTCCATTTCTCTCTC 480
Db 11920 TCGCCATGCACATGGTGTAAATTAATCTCCAGCATATCTTCTGCTTCCATTTCTCTCTC 11979
Qy 481 CCTCTTTTAAATTTGTGTTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGTAGCTACA 540
Db 11980 CCTCTTTTAAATTTGTGTTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGTAGCTACA 12039
Qy 541 ACTTAATCTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA 600
Db 12040 ACTTAATCTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA 12099
Qy 601 TTCAAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGGAAGAGCG 660
Db 11680 GCTCAGAAATTACTCTGTTTGTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 11739
```





Qy 901 CCAAACTTGAGCAACCCGGAGTCTGGATTCTGGGAAGTCTCAGCTGTCTCGGGTTGT 960  
Db 12400 CCAAACTTGAGCAACCCGGAGTCTGGATTCTGGGAAGTCTCAGCTGTCTCGGGTTGT 12459  
Qy 961 GCCGGGGCCCCAGGTCTGGAGGGGACCAAGTGGCCGTGTGGC 1001  
Db 12460 GCCGGGGCCCCAGGTCTGGAGGGGACCAAGTGGCCGTGTGGC 12500

## RESULT 10

US-10-456-830-1  
; Sequence 1, Application US/10456830  
; Publication No. US20040248246A1  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America, as  
; APPLICANT: represented by the Secretary of the Department of Health and  
; APPLICANT: Human Services  
; APPLICANT: Horikawa, Izumi  
; APPLICANT: Barrett, J. Carl  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DIFFERENTIAL EXPRESSION  
; FILE REFERENCE: 4239-63008  
; CURRENT APPLICATION NUMBER: US/10/456,830  
; CURRENT FILING DATE: 2003-06-05  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 4293  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (3545)..(3609)  
; OTHER INFORMATION: Region identical to HBV integration site in huH-4 cell line  
; FEATURE:  
; NAME/KEY: protein bind  
; LOCATION: (3729)..(3734)  
; OTHER INFORMATION: Upstream E-box  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (3916)..(3916)  
; OTHER INFORMATION: Major transcription initiation site  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (3916)..(3970)  
; OTHER INFORMATION: 5' untranslated region of mRNA  
; FEATURE:  
; NAME/KEY: protein bind  
; LOCATION: (3937)..(3942)  
; OTHER INFORMATION: Downstream E-box  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3971)..(4189)  
; OTHER INFORMATION: Exon 1  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: (4029)..(4050)  
; OTHER INFORMATION: GM2 primer binding site  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: (4190)..(4293)  
; OTHER INFORMATION: Intron 1  
US-10-456-830-1

Query Match 98.8%; Score 988.6; DB 8; Length 4293;  
Best Local Similarity 99.8%; Pred. No. 4.3e-291;  
Matches 999; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
Qy 1 GGCTGGGATTACAGGACCCGCCACCATGCCCAGCTAAATTTTGTATTTTGTAGTAGAGA 60  
Db 1927 GGCTGGGATTACAGGACCCGCCACCATGCCCAGCTAAATTTTGTATTTTGTAGTAGAGA 1986  
Qy 61 CGGGGGTGGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 120

Db 1987 CGGGGGTGGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 2046  
Qy 121 TGATCCACCTGCTCTGCCCTCTAAAGTGTCTGGGATTCAGGTTGTAGGCCACCAATGCCCCA 180  
Db 2047 TGATCCACCTGCTCTGCCCTCTAAAGTGTCTGGGATTCAGGTTGTAGGCCACCAATGCCCCA 2106  
Qy 181 GCTCAGAAATTTACTCTGTTTAAAGCAATCTGGGTCTGAGGTAGGAAGCTACCCCACTCA 240  
Db 2107 GCTCAGAAATTTACTCTGTTT - GAAACATCTGGGTCTGAGGTAGGAAGCTACCCCACTCA 2165  
Qy 241 AGTGTCTGCTGTTTAAAGCAATGATAGAAATTTTAAATTTTAAAGCAATCTCTTGA 300  
Db 2166 AGTGTCTGCTGTTTAAAGCAATGATAGAAATTTTAAATTTTAAAGCAATCTCTTGA 2225  
Qy 301 TGTTTTACACTGTGATGACTTAAGACATCATCAGCTTTTCAAGACACACACTAACTGCAACC 360  
Db 2226 TGTTTTACACTGTGATGACTTAAGACATCATCAGCTTTTCAAGACACACACTAACTGCAACC 2285  
Qy 361 ATAATCTGGGGTGTCTCTGGGTATCAGGATCTTCATTTGAATGCCGGGAGGGGTTTCC 420  
Db 2286 ATAATCTGGGGTGTCTCTGGGTATCAGGATCTTCATTTGAATGCCGGGAGGGGTTTCC 2345  
Qy 421 TCGCCATGCACATGCTGTTAAATTTACTCCAGCATAATCTCTGCTTCCATTTCTTCTCTTC 480  
Db 2346 TCGCCATGCACATGCTGTTAAATTTACTCCAGCATAATCTCTGCTTCCATTTCTTCTCTTC 2405  
Qy 481 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACACAGGTGTAAGTACA 540  
Db 2406 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACACAGGTGTAAGTACA 2465  
Qy 541 ACTTAATCTTTGTTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA 600  
Db 2466 ACTTAATCTTTGTTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA 2525  
Qy 601 TTCACAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAAGAGCG 660  
Db 2526 TTCACAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAAGAGCG 2585  
Qy 661 ACCCGTAATCCTAAGTATTTTACAAGACGAGGCTTAACCTCCAGCGAGCGTGACAGCCGAG 720  
Db 2586 ACCVGTAATCCTAAGTATTTTACAAGACGAGGCTTAACCTCCAGCGAGCGTGACAGCCGAG 2645  
Qy 721 GAGGGTGCAGGCGCTGTTCAATGCTAGCTCCATAATAAAGCAATTTCTCCGGCAGTT 780  
Db 2646 GAGGGTGCAGGCGCTGTTCAATGCTAGCTCCATAATAAAGCAATTTCTCCGGCAGTT 2705  
Qy 781 TCTGAAAGTAGGAAAGGTTACATTTTAAAGTTCGTTTGTAGCATTTTTCAGTGTTCGCCGA 840  
Db 2706 TCTGAAAGTAGGAAAGGTTACATTTTAAAGTTCGTTTGTAGCATTTTTCAGTGTTCGCCGA 2765  
Qy 841 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAAAGTTTCTCCGCCCTTAGAT 900  
Db 2766 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAAAGTTTCTCCGCCCTTAGAT 2825  
Qy 901 CCAAACTTGAGCAACCCGGAGTCTGGAATTCCTGGGAAGTCTCAGCTGTCTCGGGTTGT 960  
Db 2826 CCAAACTTGAGCAACCCGGAGTCTGGAATTCCTGGGAAGTCTCAGCTGTCTCGGGTTGT 2885  
Qy 961 GCCGGGGCCCCAGGTCTGGAGGGGACCAAGTGGCCGTGTGGC 1001  
Db 2886 GCCGGGGCCCCAGGTCTGGAGGGGACCAAGTGGCCGTGTGGC 2926

## RESULT 11

US-10-840-455-1  
; Sequence 1, Application US/10840455  
; Publication No. US20050032094A1  
; GENERAL INFORMATION:  
; APPLICANT: Bayer Aktiengesellschaft  
; APPLICANT: Hagen, Gustav  
; APPLICANT: Wick, Maresa  
; APPLICANT: Zubov, Dmitry

;; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic  
;; FILE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use  
;; FILE REFERENCE: Lea 32 805C1  
;; CURRENT APPLICATION NUMBER: US/10/840,455  
;; CURRENT FILING DATE: 2004-05-06  
;; PRIOR APPLICATION NUMBER: PCT/EP98/08216  
;; PRIOR FILING DATE: 1998-12-22  
;; PRIOR APPLICATION NUMBER: US 09/582,246  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: DE19757984.1  
;; PRIOR FILING DATE: 1997-12-24  
;; NUMBER OF SEQ ID NOS: 44  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 1  
;; LENGTH: 5126  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-840-455-1

Query Match 97.2%; Score 972.8; DB 8; Length 5126;  
Best Local Similarity 99.5%; Pred. No. 3.3e-286;  
Matches 997; Conservative 0; Mismatches 2; Indels 3; Gaps 2;

Qy 1 GGCTGGGATTACAGCACCCGCCCATGCCCAGCTAAATTTTGTATTTTGTATTTAGTAGAGA 60  
Db 3080 GGCTGGGATTACAGCACCCGCCCATGCCCAGCTAAATTTTGTATTTTGTATTTAGTAGAGA 3139

Qy 61 CGGGGGTGGGGTGGGGTCCACCATGTTGGCCAGCTGCTCGAATCTCGACTCAGA 120  
Db 3140 CGGGGGT--GGGTGGGGTTCACCATGTTGGCCAGCTGCTCGAATCTCGACTCAGA 3197

Qy 121 TGATCCACTGCCTCTGCTCTCTAAAGTCTGGGATTACAGGTGAGCCACCATGCCCA 180  
Db 3198 TGATCCACTGCCTCTGCTCTCTAAAGTCTGGGATTACAGGTGAGCCACCATGCCCA 3257

Qy 181 GCTCAGAAATTTACTCTGTTTAAACAATCTGGGTCTGAGGTAGGAAGCTACCCACTCA 240  
Db 3258 GCTCAGAAATTTACTCTGTTTAAACAATCTGGGTCTGAGGTAGGAAGCTACCCACTCA 3317

Qy 241 AGTGTGTGGTGTTTTAAAGCAATGATAGAAATTTTATTTTGTGTAGAACACTCTGA 300  
Db 3318 AGTGTGTGGTGTTTTAAAGCAATGATAGAAATTTTATTTTGTGTAGAACACTCTGA 3377

Qy 301 TGTTTTACATGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAATGCACCC 360  
Db 3378 TGTTTTACATGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAATGCACCC 3437

Qy 361 ATAATFACCTGGGGTGTCTTCTGGGTATCAGCATCTTCAATGAAATGCCGGGAGGGTTTCC 420  
Db 3438 ATAATFACCTGGGGTGTCTTCTGGGTATCAGCAATCTTCAATGAAATGCCGGGAGGGTTTCC 3497

Qy 421 TCGCCATGCATGTGTGTAAATCTCAGCATTAATCTTCTGCTTCCATTTCTTCTTTC 480  
Db 3498 TCGCCATGCATGTGTGTAAATCTCAGCATTAATCTTCTGCTTCCATTTCTTCTTTC 3557

Qy 481 CCTCTTTTAAATTTCTGTTTCTATGTTGGCTTCTCTGAGAGAACCACTAGTAAGCTACA 540  
Db 3558 CCTCTTTTAAATTTCTGTTTCTATGTTGGCTTCTCTGAGAGAACCACTAGTAAGCTACA 3617

Qy 541 ACTTAATCTTTTGTGGAAACAAATTTTCAAACCGCCCTTTTGCCTAGTGGCAGAGACAA 600  
Db 3618 ACTTAATCTTTTGTGGAAACAAATTTTCAAACCGCCCTTTTGCCTAGTGGCAGAGACAA 3677

Qy 601 TTCACAAACAGACCCCTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCG 660  
Db 3678 TTCACAAACAGACCCCTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCG 3737

Qy 661 ACCCGTAACTCTAAGTATTTTAAAGCGAGGCTTAACCTCCAGCGAGCGTACAGCCGAGG 720  
Db 3738 ACCCGTAACTCTAAGTATTTTAAAGCGAGGCTTAACCTCCAGCGAGCGTACAGCCGAGG 3797

Qy 721 GAGGGTGGAGGCGCTGTTTCAATGCTAGCTCCATAATAAAGCAATTTTCTCCGCGAGTT 780

Db 3798 GAGGGTCGAGGGCCTGTTCAAAATGCTAGCTCCATAAATAAAGCAATTTCTCCGCGAGTT 3857

Qy 781 TCTGAAAGTAGGAAAGGTTACATTTAAAGGTTGCGTTTGTAGCAATTTTCAGTGTTTGCCGA 840

Db 3858 TCTGAAAGTAGGAAAGGTTACATTTAAAGGTTGCGTTTGTAGCAATTTTCAGTGTTTGCCGA 3917

Qy 841 CCTCAGCTACAGCATCCTCGAAGGCTTCGAGGACCCAGAGTTTCTCG--CCCTTAGA 899

Db 3918 CCTCAGCTACAGCATCCTCGAAGGCTTCGAGGACCCAGAGTTTCTCGCCCTTAGA 3977

Qy 900 TCCAAACTTTCAGCAACCCGAGTCTGGATTCTCTGGAGTCTCAGCTGTCTCTCGGTTG 959

Db 3978 TCCAAACTTTCAGCAACCCGAGTCTGGATTCTCTGGAGTCTCAGCTGTCTCTCGGTTG 4037

Qy 960 TGCCGGGGCCCCAGGCTCTGGAGGGGACCGAGTGGCGCGTGTGGC 1001

Db 4038 TGCCGGGGCCCCAGGCTCTGGAGGGGACCGAGTGGCGCGTGTGGC 4079

RESULT 12  
US-10-840-455-3  
; Sequence 3, Application US/10840455  
; Publication No. US20050032094A1  
; GENERAL INFORMATION:  
; APPLICANT: Bayer Aktiengesellschaft  
; APPLICANT: Hagen, Gustav  
; APPLICANT: Wick, Maresa  
; APPLICANT: Zubov, Dmitry  
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic  
; FILE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use  
; FILE REFERENCE: Lea 32 805C1  
; CURRENT APPLICATION NUMBER: US/10/840,455  
; PRIOR FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: PCT/EP98/08216  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: US 09/582,246  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: DE19757984.1  
; PRIOR FILING DATE: 1997-12-24  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 11276  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-840-455-3

Query Match 97.2%; Score 972.8; DB 8; Length 11276;  
Best Local Similarity 99.5%; Pred. No. 5e-286;  
Matches 997; Conservative 0; Mismatches 2; Indels 3; Gaps 2;

Qy 1 GGCTGGGATTACAGCACCCGCCCATGCCCAGCTAAATTTTGTATTTTGTATTTAGTAGAGA 60  
Db 9230 GGCTGGGATTACAGCACCCGCCCATGCCCAGCTAAATTTTGTATTTTGTATTTAGTAGAGA 9289

Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGCTGCTCGAATCTTCTGACCTCAGA 120  
Db 9290 CGGGGGT--GGGTGGGGTTCACCATGTTGGCCAGCTGCTCGAATCTTCTGACCTCAGA 9347

Qy 121 TGATCCACTGCCTCTGCTCTCTAAAGTCTGGGATTACAGGTGAGCCACCATGCCCA 180  
Db 9348 TGATCCACTGCCTCTGCTCTCTAAAGTCTGGGATTACAGGTGAGCCACCATGCCCA 9407

Qy 181 GCTCAGAAATTTACTCTGTTTAAAGCAATCTGAGGTCTGAGGTAGGAAGCTCACCCACTCA 240  
Db 9408 GCTCAGAAATTTACTCTGTTTAAAGCAATCTGAGGTCTGAGGTAGGAAGCTCACCCACTCA 9467

Qy 241 AGTGTGTGGTGTTTTAAAGCAATCTGATAGAAATTTTATTTTGTGTAGAACACTCTTGA 300  
Db 9468 AGTGTGTGGTGTTTTAAAGCAATCTGATAGAAATTTTATTTTGTGTAGAACACTCTTGA 9527

Qy 301 TGTTTTACATGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAATCTGACCC 360

Db 9528 TGTGTTTACATGTCATGAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 9587  
Qy 361 ATATATCTGGGGTCTCTTCTGGGTATCAGCGATCTTCATTTGAATGCCGGAGGGGTTTCC 420  
Db 9588 ATATATCTGGGGTCTCTTCTGGGTATCAGCAATCTTCATTTGAATGCCGGAGGGGTTTCC 9647  
Qy 421 TCGCCATGCACATCGTGTAAATTAATCTCAGCATAACTCTTCGCTTCCATTTCTCTCTTC 480  
Db 9648 TCGCCATGCACATCGTGTAAATTAATCTCAGCATAACTCTTCGCTTCCATTTCTCTCTTC 9707  
Qy 481 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACAGTGTAGCTACA 540  
Db 9708 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACAGTGTAGCTACA 9767  
Qy 541 ACTTAACCTTTGTTGGAAACAAATTTTCAAACCCGCCCTTTGCCCTTAGTGGCAGACAA 600  
Db 9768 ACTTAACCTTTGTTGGAAACAAATTTTCAAACCCGCCCTTTGCCCTTAGTGGCAGACAA 9827  
Qy 601 TTCACAAACACAGCCCTTTTAAAGAGCTTAGGGATCACTAAGGGGATTTCTAGAAGAGCG 660  
Db 9828 TTCACAAACACAGCCCTTTTAAAGAGCTTAGGGATCACTAAGGGGATTTCTAGAAGAGCG 9887  
Qy 661 ACCGTAATCTTAAGTATTTTACAAGACGAGCTTAACCTTCAGCGAGCGTGACGCCAGG 720  
Db 9888 ACCGTAATCTTAAGTATTTTACAAGACGAGCTTAACCTTCAGCGAGCGTGACGCCAGG 9947  
Qy 721 GAGGGTCGGAGCGCTGTTCAAATGCTAGCTTCATTAATTAAGCAATTTCTCCGGCAGTT 780  
Db 9948 GAGGGTCGGAGCGCTGTTCAAATGCTAGCTTCATTAATTAAGCAATTTCTCCGGCAGTT 10007  
Qy 781 TCTCAAAAGTAGGAAGGTTACATTTAAGTTGCGTTGTTAGCAATTTCAAGTTTTCGCGA 840  
Db 10008 TCTCAAAAGTAGGAAGGTTACATTTAAGTTGCGTTGTTAGCAATTTCAAGTTTTCGCGA 10067  
Qy 841 CCTCAGCTACAGCATCCTCGAAGCCTCGGAGACCCAGAGTTTCTCG-CCCTTTAGA 899  
Db 10068 CCTCAGCTACAGCATCCTCGAAGCCTCGGAGACCCAGAGTTTCTCGCCCTTTAGA 10127  
Qy 900 TCMAACTTGAGCAACCCGGAGTCTGATTCCTGGGAAGTCTCAGCTGCTCGGGTTG 959  
Db 10128 TCMAACTTGAGCAACCCGGAGTCTGATTCCTGGGAAGTCTCAGCTGCTCGGGTTG 10187  
Qy 960 TGCCGGGGCCCCAGGCTCTGGAGGGGACAGTGGCCGCTGTGCG 1001  
Db 10188 TGCCGGGGCCCCAGGCTCTGGAGGGGACAGTGGCCGCTGTGCG 10229

RESULT 13  
US-10-840-455-43  
; Sequence 43, Application US/10840455  
; Publication No. US20050032094A1  
; GENERAL INFORMATION:  
; APPLICANT: Bayer Aktiengesellschaft  
; APPLICANT: Hagen, Gustav  
; APPLICANT: Wick, Mareisa  
; APPLICANT: Zubov, Dmitry  
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic  
; FILE REFERENCE: Telomerase Subunit, and Their Diagnostic and Therapeutic Use  
; CURRENT APPLICATION NUMBER: US/10/840,455  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: PCT/EP98/08216  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: US 09/582,246  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: DE19757984.1  
; PRIOR FILING DATE: 1997-12-24  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 43  
; LENGTH: 26414  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-10-840-455-43  
Query Match 97.2%; Score 972.8; DB 8; Length 26414;  
Best Local Similarity 99.5%; Pred. No. 7.9e-286;  
Matches 997; Conservative 0; Mismatches 2; Indels 3; Gaps 2;  
Qy 1 GGCCTGGGATTTACAGGACCCGCCACATGCGCCAGCTAAATTTTGTATTTTGTAGTACAGA 60  
Db 9230 GGCCTGGGATTTACAGGACCCGCCACATGCGCCAGCTAAATTTTGTATTTTGTAGTACAGA 9289  
Qy 61 CGGGGGTGGGGGTTTCAATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 120  
Db 9290 CGGGGGT--GGTGGGGTTTCAATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 9347  
Qy 121 TGATCCACTGCTCTGCTCTTAAAGTGTCTGGGATTTACAGGTGTGAGCCACCATGCCCCA 180  
Db 9348 TGATCCACTGCTCTGCTCTTAAAGTGTCTGGGATTTACAGGTGTGAGCCACCATGCCCCA 9407  
Qy 181 GCTCAGAAATTTACTCTGTTTAAAGAAATCTGGGTCTGAGGTAGGAGCTCACCCACTCA 240  
Db 9408 GCTCAGAAATTTACTCTGTTTAAAGAAATCTGGGTCTGAGGTAGGAGCTCACCCACTCA 9467  
Qy 241 AGTGTGCTGCTGTTTAAAGCAATGATAGAAATTTTATTTGTTGTTAGAACACTCTTGA 300  
Db 9468 AGTGTGCTGCTGTTTAAAGCAATGATAGAAATTTTATTTGTTGTTAGAACACTCTTGA 9527  
Qy 301 TGTGTTTACATCTGATGATGATTAAGCATCATCAGCTTTTCAAAGACACACTAACTGACCC 360  
Db 9528 TGTGTTTACATCTGATGATGATTAAGCATCATCAGCTTTTCAAAGACACACTAACTGACCC 9587  
Qy 361 ATAATCTGCGGTGCTCTTCTGGGTATCAGCGATCTTCATTTGAATGCCGGAGGGGTTTCC 420  
Db 9588 ATAATCTGCGGTGCTCTTCTGGGTATCAGCAATCTTCATTTGAATGCCGGAGGGGTTTCC 9647  
Qy 421 TCGCCATGCACATGCTGTTAAATTAATCTCAGCATAACTCTTCTGCTTCCATTTCTCTCTTC 480  
Db 9648 TCGCCATGCACATGCTGTTAAATTAATCTCAGCATAACTCTTCTGCTTCCATTTCTCTCTTC 9707  
Qy 481 CTTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGTAGCTACACA 540  
Db 9708 CTTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGTAGCTACACA 9767  
Qy 541 ACTTAACCTTTGTTGGAAACAAATTTTCAAACCCGCCCTTTGCCCTTAGTGGCAGACAA 600  
Db 9768 ACTTAACCTTTGTTGGAAACAAATTTTCAAACCCGCCCTTTGCCCTTAGTGGCAGACAA 9827  
Qy 601 TTCACAAACACAGCCCTTTTAAAGAGCTTAGGGATCACTAAGGGGATTTCTAGAAGAGCG 660  
Db 9828 TTCACAAACACAGCCCTTTTAAAGAGCTTAGGGATCACTAAGGGGATTTCTAGAAGAGCG 9887  
Qy 661 ACCGTAATCTTAAGTATTTTACAAGACGAGCTTAACCTTCAGCGAGCGTGACGCCAGG 720  
Db 9888 ACCTGTAATCTTAAGTATTTTACAAGACGAGGCTAACCTTCAGCGAGCGTGACGCCAGG 9947  
Qy 721 GAGGGTCGGAGCGCTGTTCAAATGCTAGCTTCATTAATTAAGCAATTTCTCCGGCAGTT 780  
Db 9948 GAGGGTCGGAGCGCTGTTCAAATGCTAGCTTCATTAATTAAGCAATTTCTCCGGCAGTT 10007  
Qy 781 TCTGAAAGTAGGAAGGTTACATTTAAGTTGCGTTTGTGTTAGCAATTTCAAGTGTTCGCGA 840  
Db 10008 TCTGAAAGTAGGAAGGTTACATTTAAGTTGCGTTTGTGTTAGCAATTTCAAGTGTTCGCGA 10067  
Qy 841 CTTCAGCTACAGCATCCTCGAAGCCTCGGAGACCCAGAGTTTCTCG-CCCTTTAGA 899  
Db 10068 CTTCAGCTACAGCATCCTCGAAGCCTCGGAGACCCAGAGTTTCTCGCCCTTTAGA 10127  
Qy 900 TCCAAACTTGAGCAACCCGGAGTCTGATTCCTGGGAAGTCTCAGCTGCTCGGGTTG 959  
Db 10128 TCCAAACTTGAGCAACCCGGAGTCTGATTCCTGGGAAGTCTCAGCTGCTCGGGTTG 10187  
Qy 960 TGCCGGGGCCCCAGGCTCTGGAGGGGACAGTGGCCGCTGTGCG 1001  
Db 10188 TGCCGGGGCCCCAGGCTCTGGAGGGGACAGTGGCCGCTGTGCG 10229

RESULT 14  
US-09-733-294A-30  
Sequence 30, Application US/09733294A  
Patent No. US20020045588A1  
GENERAL INFORMATION:  
APPLICANT: Brett P. Monia  
APPLICANT: William M. Gaarde  
APPLICANT: Susan M. Freier  
APPLICANT: Edward V. Wanciewicz  
TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION  
FILE REFERENCE: ISPH-0527  
CURRENT FILING DATE: 2000-12-07  
PRIOR APPLICATION NUMBER: 09/572,423  
PRIOR FILING DATE: 2000-05-16  
NUMBER OF SEQ ID NOS: 108  
SEQ ID NO 30  
LENGTH: 51552  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: exon  
LOCATION: (1)...(11492)  
OTHER INFORMATION: exon 1  
NAME/KEY: intron  
LOCATION: (11493)...(11596)  
OTHER INFORMATION: intron 1  
NAME/KEY: exon  
LOCATION: (11597)...(12950)  
OTHER INFORMATION: exon 2  
NAME/KEY: intron  
LOCATION: (12951)...(21566)  
OTHER INFORMATION: intron 2  
NAME/KEY: exon  
LOCATION: (21567)...(21762)  
OTHER INFORMATION: exon 3  
NAME/KEY: intron  
LOCATION: (21763)...(23851)  
OTHER INFORMATION: intron 3  
NAME/KEY: exon  
LOCATION: (23852)...(24032)  
OTHER INFORMATION: exon 4  
NAME/KEY: intron  
LOCATION: (24033)...(24719)  
OTHER INFORMATION: intron 4  
NAME/KEY: exon  
LOCATION: (24720)...(24899)  
OTHER INFORMATION: exon 5  
NAME/KEY: intron  
LOCATION: (24900)...(25393)  
OTHER INFORMATION: intron 5  
NAME/KEY: exon  
LOCATION: (25394)...(25549)  
OTHER INFORMATION: exon 6  
NAME/KEY: intron  
LOCATION: (25550)...(30196)  
OTHER INFORMATION: intron 6  
NAME/KEY: exon  
LOCATION: (30197)...(30292)  
OTHER INFORMATION: exon 7  
NAME/KEY: intron  
LOCATION: (30293)...(31272)  
OTHER INFORMATION: intron 7  
NAME/KEY: exon  
LOCATION: (31273)...(31358)  
OTHER INFORMATION: exon 8  
NAME/KEY: intron  
LOCATION: (31359)...(33843)  
OTHER INFORMATION: intron 8  
NAME/KEY: unsure  
LOCATION: 31450

OTHER INFORMATION: unknown  
NAME/KEY: exon  
LOCATION: (33844)...(33957)  
OTHER INFORMATION: exon 9  
NAME/KEY: intron  
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OTHER INFORMATION: exon 10  
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OTHER INFORMATION: intron 10  
NAME/KEY: exon  
LOCATION: (37885)...(38073)  
OTHER INFORMATION: exon 11  
NAME/KEY: intron  
LOCATION: (38074)...(41874)  
OTHER INFORMATION: intron 11  
NAME/KEY: exon  
LOCATION: (41875)...(42001)  
OTHER INFORMATION: exon 12  
NAME/KEY: intron  
LOCATION: (42002)...(42881)  
OTHER INFORMATION: intron 12  
NAME/KEY: exon  
LOCATION: (42882)...(42943)  
OTHER INFORMATION: exon 13  
NAME/KEY: intron  
LOCATION: (42944)...(46129)  
OTHER INFORMATION: intron 13  
NAME/KEY: exon  
LOCATION: (46130)...(46254)  
OTHER INFORMATION: exon 14  
NAME/KEY: intron  
LOCATION: (46255)...(47035)  
OTHER INFORMATION: intron 14  
NAME/KEY: exon  
LOCATION: (47036)...(47173)  
OTHER INFORMATION: exon 15  
NAME/KEY: intron  
LOCATION: (47174)...(47709)  
OTHER INFORMATION: intron 15  
NAME/KEY: exon  
LOCATION: (47710)...(50544)  
OTHER INFORMATION: exon 16  
US-09-733-294A-30

Query Match 97.2%; Score 972.8; DB 3; Length 51552;  
Best Local Similarity 99.5%; Pred. No. 1.1e-285;  
Matches 997; Conservative 0; Mismatches 2; Indels 3; Gaps 2;  
QY 1 GGCTGGGATTACAGGCACCCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGA 60  
DB 9230 GGCTGGGATTACAGGCACCCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGA 9289  
QY 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGCTGCTCGAATCTTCACCTCAGA 120  
DB 9290 CGGGGGT--GGGTGGGGTTCACCATGTTGGCCAGCTGCTCGAATCTTCACCTCAGA 9347  
QY 121 TGATCCACTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 180  
DB 9348 TGATCCACTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 9407  
QY 181 GCTCAGAAATTACTCTGTTTGAACAACATCTGGGTCTGAGGTAGGAAGCTCACCCACTCA 240  
DB 9408 GCTCAGAAATTACTCTGTTTGAACAACATCTGGGTCTGAGGTAGGAAGCTCACCCACTCA 9467  
QY 241 AGTGTGTGGTGTGTTTAAAGCAATCATAGAAATTTTATTTTCTTAAACACTCTTGA 300  
DB 9468 AGTGTGTGGTGTGTTTAAAGCAATCATAGAAATTTTATTTTCTTAAACACTCTTGA 9527  
QY 301 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAGACACACTACTGACCC 360

Db 9528 TGTTTACATGATGACCTAAGACATCATCAGCTTTTCAAGACACACTAATGACCC 9587  
Qy 361 ATAACTCGGGGTCTCTTGGGTATCAGCATCTTCATTGAATGCGGGAGCGTTTCC 420  
Db 9588 ATAACTCGGGGTCTCTTGGGTATCAGCAATCTTCATTGAATGCGGGAGCGTTTCC 9647  
Qy 421 TCGCATGACATGGTGTAACTACTCCAGCATATCTTCGCTTCAATTTCTCTTTC 480  
Db 9648 TCGCATGACATGGTGTAACTACTCCAGCATATCTTCGCTTCAATTTCTCTTTC 9707  
Qy 481 CCTCTTTAAATGTGTCTTCTATGTGGCTTCTGCGAGAGAACAGTGAAGTACA 540  
Db 9708 CCTCTTTAAATGTGTCTTCTATGTGGCTTCTGCGAGAGAACAGTGAAGTACA 9767  
Qy 541 ACTTAATCTTTGTGGAAACAAATTTTCAAACCGCCCTTTGCGCTAGTGGCAGACAA 600  
Db 9768 ACTTAATCTTTGTGGAAACAAATTTTCAAACCGCCCTTTGCGCTAGTGGCAGACAA 9827  
Qy 601 TTCACAAACACAGCCCTTTAAAGGCTTAAAGGATCACTAAGGGATTTCTAGNAGCG 660  
Db 9828 TTCACAAACACAGCCCTTTAAAGGCTTAAAGGATCACTAAGGGATTTCTAGNAGCG 9887  
Qy 661 ACCGTAATCTTAAGTATTTTACAAGACAGGCTAACTCCAGCGAGCGTGACAGCCGAGG 720  
Db 9888 ACCTGTAATCTTAAGTATTTTACAAGACAGGCTAACTCCAGCGAGCGTGACAGCCGAGG 9947  
Qy 721 GAGGTCGAGGCTGTTCAAATGCTAGCTCCATAATAAGCAATTTCTCCGCGCAGTT 780  
Db 9948 GAGGTCGAGGCTGTTCAAATGCTAGCTCCATAATAAGCAATTTCTCCGCGCAGTT 10007  
Qy 781 TCTGAAGTAGGAAGGTATCAATTAAGTTGCGTTTGTAGCAATTCAGTGTTCGCGA 840  
Db 10008 TCTGAAGTAGGAAGGTATCAATTAAGTTGCGTTTGTAGCAATTCAGTGTTCGCGA 10067  
Qy 841 CCTCAGCTACAGCATCCTGCAAGGCTCGGGAGACCCAGAGTTTCTCG-CCCTTGA 899  
Db 10068 CCTCAGCTACAGCATCCTGCAAGGCTCGGGAGACCCAGAGTTTCTCGCCCTTGA 10127  
Qy 900 TCCAACTTGAGCAACCCGAGTCTGATTCCTGGGAAGTCTCAGCTGCTCGCGTTG 959  
Db 10128 TCCAACTTGAGCAACCCGAGTCTGATTCCTGGGAAGTCTCAGCTGCTCGCGTTG 10187  
Qy 960 TCGCGGGCCCCAGTCTGAGGGGACAGTGGCGGTGTGCG 1001  
Db 10188 TCGCGGGCCCCAGTCTGAGGGGACAGTGGCGGTGTGCG 10229

RESULT 15

US-10-877-124-6

; Sequence 6, Application US/10877124

; Publication No. US20040242529A1

; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Morin, Gregg B.

; Harley, Calvin B.

; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/877,124

FILING DATE: 24-Jun-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503

FILING DATE: 02-Nov-1999

APPLICATION NUMBER: 08/974,549

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/844,419

FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US/08/846,017

FILING DATE: 25-Apr-1997

APPLICATION NUMBER: US/08/851,843

FILING DATE: 06-May-1997

APPLICATION NUMBER: US/08/854,050

FILING DATE: 09-May-1997

APPLICATION NUMBER: US/08/911,312

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US/08/912,951

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US/08/915,503

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-Oct-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-Oct-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 4335 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: -

LOCATION: 1..4335

OTHER INFORMATION: /note= "genomic DNA insert of pGRN14"

FEATURE:

NAME/KEY: intron

LOCATION: 2715..2818

OTHER INFORMATION: /note= "intron 1"

FEATURE:

NAME/KEY: intron

LOCATION: 4173..4326

OTHER INFORMATION: /note= "intron 2"

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-877-124-6

Query Match 93.0%; Score 930.8; DB 8; Length 4335;

Best Local Similarity 99.1%; Pred. No. 2.2e-273;

Matches 999; Conservative 0; Mismatches 2; Indels 7; Gaps 6;

Qy 1 GGCTGGGATTACAGGCACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGA 60

Db 438 GGCTGGGATTACAGGCACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGA 497

Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 120

Db 498 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 557

Qy 121 TGATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCA 180

Db 558 TGATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCA 617



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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 11:12:13 ; Search time 210.333 Seconds  
(without alignments)  
3469.703 Million cell updates/sec

Title: US-09-615-039-1\_COPY\_11500\_12500  
Perfect score: 1001  
Sequence: 1 ggcctgggattacagccacc.....gggaccagtggcgtgtggc 1001

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4637633 seqs, 364532575 residues

Total number of hits satisfying chosen parameters: 9275266

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:  
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2: /cgm2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
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4: /cgm2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
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10: /cgm2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132.8	13.3	152335	7	US-11-121-086-73
2	131	13.1	130472	6	US-10-995-561-13312
3	129.8	13.0	146656	7	US-11-121-086-68
4	128.4	12.8	167116	7	US-11-121-086-44
5	128	12.8	14670	6	US-10-995-561-13328
6	128	12.8	18895	6	US-10-995-561-13329
7	127.8	12.8	110711	6	US-10-995-561-13264
8	127.6	12.7	153142	7	US-11-121-086-27
9	127.6	12.7	203467	7	US-11-121-086-50
10	127	12.7	319608	7	US-11-155-492-1
11	127	12.7	319608	7	US-11-145-703-1
12	126.6	12.6	16843	6	US-10-995-561-13302
13	126.6	12.6	18238	6	US-10-995-561-13386
14	126.2	12.6	201	6	US-10-995-561-133560
15	125.8	12.6	175023	7	US-11-121-086-18
16	125.4	12.5	168656	7	US-11-112-908-59
17	125.4	12.5	170285	7	US-11-112-908-58
18	125.4	12.5	180862	7	US-11-112-908-40
19	125.2	12.5	40644	6	US-10-995-561-13480
20	124.8	12.5	159497	7	US-11-112-908-61
21	124.8	12.5	165857	7	US-11-121-086-34
22	124.8	12.5	171427	7	US-11-112-908-60
23	124.6	12.4	98716	6	US-10-995-561-13331

24	124.4	12.4	195998	6	US-10-995-561-13489
c 25	124.4	12.4	1080000	6	US-10-928-446A-1
c 26	124.4	12.4	1080000	6	US-10-928-446A-181
c 27	124.4	12.4	1080000	6	US-10-928-446A-183
c 28	124.4	12.4	1080000	6	US-10-928-446A-185
c 29	124.4	12.4	1080000	6	US-10-928-446A-187
c 30	124.4	12.4	1080000	6	US-10-928-446A-189
c 31	124.4	12.4	1080000	6	US-10-928-446A-191
c 32	124.4	12.4	1080000	6	US-10-928-446A-193
c 33	124.4	12.4	1080000	6	US-10-928-446A-195
c 34	124.4	12.4	1080000	6	US-10-928-446A-197
c 35	124.4	12.4	1080000	6	US-10-928-446A-199
c 36	124.4	12.4	1080000	6	US-10-928-446A-201
37	124.2	12.4	161994	7	US-11-112-908-57
38	123.8	12.4	125594	6	US-10-658-986-5
39	123.6	12.3	201990	6	US-10-995-561-13303
c 40	123.4	12.3	159138	6	US-10-995-561-13230
c 41	123	12.3	120697	7	US-11-121-086-48
c 42	123	12.3	175416	7	US-11-121-086-43
c 43	122.8	12.3	137000	6	US-10-515-538-11
c 44	122.2	12.2	201	6	US-10-995-561-33666
c 45	122.2	12.2	67126	6	US-10-995-561-13342

ALIGNMENTS

RESULT 1  
US-11-121-086-73  
; Sequence 73, Application US/11121086  
; Publication No. US2005026459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121.086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 73  
; LENGTH: 152335  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-121-086-73

Query Match	13.3%	Score 132.8;	DB 7;	Length 152335;
Best Local Similarity	81.1%	Pred. No. 5.9e-30;		
Matches 167;	Conservative 0;	Mismatches 37;	Indels 2;	Gaps 1;
QY	2	GCTGGATTACAGGACCCGCCACATGCCAGCTAA--TTTTTGTATTTTAGTAGAG 59		
Db	84893	GCTGGATTATAGCACCCTGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAG 84952		
QY	60	ACGGGGTGGGGTGGGCTTACCATGTGGCAGGCTGCTCGAACTTCGACCTCAG 119		
Db	84953	ACAAATGGGTATATGGGTTTCCCATGTGGCAGGTTGGTCTCGAACTTCGACCTCAG 85012		
QY	120	ATGATCCACCTGCCTCTGCCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCC 179		
Db	85013	GTGATCCACCTGCCTCTGCCTCTCCCAAGTCTGGGATTACAGGCTGAGCCACTGTGCC 85072		
QY	180	AGCTCAGAAATTTACTCTCTTTTAGAAA 205		
Db	85073	AGCCGATTACTGTAGTTTATAGTAA 85098		

RESULT 2  
US-10-995-561-13312  
; Sequence 13312, Application US/10995561  
; Publication No. US20050272054A1

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; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13312
; LENGTH: 130472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13312

Query Match      13.1%; Score 131; DB 6; Length 130472;
Best Local Similarity 84.1%; Pred. No. 2e-29;
Matches 164; Conservative 0; Mismatches 20; Indels 11; Gaps 1;

QY      2 GCTGGGATTACAGCAGCCCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGAC 61
Db      85026 GCTGGGATTACAGCGCCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGAT 85085

QY      62 GGGGGTGGGGTGGGGTTCCACATGTTGGCCAGGCTGTCTCGAACTTCTGACCTCAGAT 121
Db      85086 G-----GGGCTTCACATGTTGGCCAGACTGTCTCGAACTTCTGACCTCAGGT 85134

QY      122 GATCCACTGCTCTGCTCTCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCAG 181
Db      85135 GATCCACCGCTCAGCTCTCCAAAGTCTGTGATTACAGGCGTGAGCCACCGCACCCAG 85194

QY      182 CTCAGATTTACTCT 196
Db      85195 CCATGATTTGACTCT 85209

RESULT 3
US-11-121-086-68/c
; Sequence 68, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; PRIOR FILING DATE: 2005-05-04
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68
; LENGTH: 146656
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-68

Query Match      13.0%; Score 129.8; DB 7; Length 146656;
Best Local Similarity 78.3%; Pred. No. 5e-29;
Matches 173; Conservative 0; Mismatches 37; Indels 11; Gaps 1;

QY      2 GCTGGGATTACAGCAGCCCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGAC 61
Db      93223 GCTGGGACTACAGCAGCCCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGAT 93164

QY      62 GGGGGTGGGGTGGGGTTCCACATGTTGGCCAGGCTGTCTCGAACTTCTGACCTCAGAT 121
Db      93163 G-----GAGTTTCACCATATTGGCCAGGCTGTCTGAACTTCTGGCTCAAT 93115

QY      122 GATCCACTGCTCTGCTCTCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCAG 181
Db      93114 GACCCACTGCTCTGGGCTCTCAAAGTCTGGGATTACTGTGTGAGCCACTGTGCCAG 93055
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QY      182 CTCAGATTTACTCTGTTTAGAAACATCTGGGTCTAGGTA 222
Db      93054 CCTAAATGTATGTGTTATTATTAAGCCACTCAATTTGAGGTA 93014

RESULT 4
US-11-121-086-44
; Sequence 44, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; PRIOR FILING DATE: 2005-05-04
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 167116
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-44

Query Match      12.8%; Score 128.4; DB 7; Length 167116;
Best Local Similarity 76.3%; Pred. No. 1.5e-28;
Matches 171; Conservative 0; Mismatches 51; Indels 2; Gaps 1;

QY      2 GCTGGGATTACAGCAGCCCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGAC 61
Db      35913 GCTGGGATTACAGGCGATGCGCCACCATGCCCGGCTAATTTTA--TATTTTAGTAGAGAC 35970

QY      62 GGGGGTGGGGTGGGGTTCCACATGTTGGCCAGGCTGTCTCGAACTTCTGACCTCAGAT 121
Db      35971 AGGGTTGAGATGGGGTTCTCCATGTTGGTCAGGCTGGTCTCGAACTTCTGAGCTCAGGT 36030

QY      122 GATCCACTGCTCTGCTCTCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCAG 181
Db      36031 GATCCGCTGCTCTCAGCTCCCAAAGTCTGGGATTATAGGCGTGAGCCACTGTACCCGG 36090

QY      182 CTCAGATTTACTCTGTTTAGAAACATCTGGGTCTAGGTTAGGA 225
Db      36091 CCTGTAGTTTTCATCATATAATAGTCTGTGTCATGTTTGTGTAGA 36134
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RESULT 5
US-10-995-561-13328
; Sequence 13328, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13328
; LENGTH: 14670
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13328

Query Match      12.8%; Score 128; DB 6; Length 14670;
Best Local Similarity 85.3%; Pred. No. 4.7e-29;
Matches 157; Conservative 1; Mismatches 16; Indels 10; Gaps 1;

QY      2 GCTGGGATTACAGCAGCCCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGAC 61
```

```
Db 3515 GCTGGGATTACAGGACCCGCCACCCAGCGGCTCATTTTGTATTTTAGTAGAGAC 3574
Qy 62 GGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGAT 121
Db 3575 GGGGGT-----TTACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGGT 3624
Qy 122 GATCACCTGCTCTGCTCTCTAAAGTGCTGGGATTACAGGTGTGAGCCACCATGCCAG 181
Db 3625 GATCACCCGCTAGGCTCTCCAAAGTGCTGGGATACAGYGTGAGCCACCGCGCGG 3684
Qy 182 CTCA 185
Db 3685 CTTA 3688

RESULT 6
US-10-995-561-13329/c
; Sequence 13329, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13329
; LENGTH: 18895
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-995-561-13329

Query Match 12.8%; Score 128; DB 6; Length 18895;
Best Local Similarity 85.3%; Pred. No. 5.5e-29;
Matches 157; Conservative 1; Mismatches 16; Indels 10; Gaps 1;

Qy 2 GCTGGGATTACAGGACCCGCCACCCAGCGGCTCATTTTGTATTTTAGTAGAGAC 61
Db 17066 GCTGGGATTACAGGACCCGCCACCCAGCGGCTCATTTTGTATTTTAGTAGAGAC 17007
Qy 62 GGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGAT 121
Db 17006 GGGGGT-----TTACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGGT 16957
Qy 122 GATCACCTGCTCTGCTCTCTAAAGTGCTGGGATTACAGGTGTGAGCCACCATGCCAG 181
Db 16956 GATCACCCGCTAGGCTCTCCAAAGTGCTGGGATACAGYGTGAGCCACCGCGCGG 16897
Qy 182 CTCA 185
Db 16896 CTTA 16893

RESULT 7
US-10-995-561-13264
; Sequence 13264, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13264
; LENGTH: 110711
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)....(110711)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-10-995-561-13264)

Query Match 12.8%; Score 127.8; DB 6; Length 110711;
Best Local Similarity 81.4%; Pred. No. 1.8e-28;
Matches 162; Conservative 2; Mismatches 24; Indels 11; Gaps 1;

Qy 2 GCTGGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 61
Db 32714 GCTGGGATTACAGGACCGCCACCATGCCCGGCTAAATTTTGTATTTTAGTAGAGAC 32773
Qy 62 GGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGAT 121
Db 32774 -----AGGGTTTCASCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGGT 32822
Qy 122 GATCACCTGCTCTGCTCTCTAAAGTGCTGGGATTACAGGTGTGAGCCACCATGCCAG 181
Db 32823 GATCACCTGCTGCTGGGCTCCAAAGTGTTAGGATTACAGGTGTGAGCCACCATGCCAG 32882
Qy 182 CTCAGAAATTTACTCTGTTT 200
Db 32883 CCTACAGTAGTAACCTTTT 32901

RESULT 8
US-11-121-086-27/c
; Sequence 27, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 153142
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-086-27

Query Match 12.7%; Score 127.6; DB 7; Length 153142;
Best Local Similarity 80.6%; Pred. No. 2.5e-28;
Matches 166; Conservative 0; Mismatches 29; Indels 11; Gaps 1;

Qy 2 GCTGGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 61
Db 102935 GCTGGGATTACAGGCTGCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 102876
Qy 62 GGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGAT 121
Db 102875 G-----GGGTTTCAATGTTGGCCAGGTTGCTTGAACCTCTGACCTCAGGT 102827
Qy 122 GATCACCTGCTCTGCTCTCTAAAGTGCTGGGATTACAGGTGTGAGCCACCATGCCAG 181
Db 102826 GATCACCTGCTCTGCTCTCTAAAGTGCTGGGATTACAGGCGTGAGCCACCATGCCAGT 102767
Qy 182 CTCAGAAATTTACTCTGTTTAGAACA 207
Db 102766 CTCATTTTGTATTTTAAAGAGA 102741

RESULT 9
US-11-121-086-50/c
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```
; Sequence 50, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50
; LENGTH: 203467
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-086-50

Query Match      12.7%; Score 127.6; DB 7; Length 203467;
Best Local Similarity 77.5%; Pred. No. 3e-28;
Matches 172; Conservative 0; Mismatches 39; Indels 11; Gaps 1;

Qy      2 GCTGGGATTACAGGCACCGCCACCATGCTCCAGCTAAATTTTGTATTTTAGTAGAGAC 61
Db      143904 GCTGGGATTACAGGTGCTGCACACCGCCGCTAATTTTGTATTTTAGTAGAGAT 143845

Qy      62 GGGGGTGGGGTGGGGTTTACCATGTTGGCCAGCGTGTCTCGAACTTCTGACCTCAGAT 121
Db      143844 G-----GGGTTTCAATATGTTGGCCAGCGTGTCTTGAACCTCTGACCTCAGGA 143796

Qy      122 GATCCACTGCTCTGCTCTCTTAAGTCTGGGATTACAGGTGAGCCACCATGCCAG 181
Db      143795 GATCCACCGCTCGGCTCTCCAAAGTCTCAGATTACAGCGTGAGCCACCGTGCCTGG 143736

Qy      182 CTCAGAAATTTACTCTGTTTAGAAACATCTGGTCTGAGGTAG 223
Db      143735 CCCCCATTTTTTTTTTTTATATTCATTTATTTCAGAGGGAG 143694

RESULT 10
US-11-155-492-1/c
; Sequence 1, Application US/11155492
; Publication No. US20050266479A1
; GENERAL INFORMATION:
; APPLICANT: Weissenbach, Jean
; APPLICANT: Hazan, Jamil
; TITLE OF INVENTION: CLONING, EXPRESSION AND CHARACTERIZATION OF THE SPGA
; TITLE OF INVENTION: GENE RESPONSIBLE FOR THE MOST COMMON FORM OF AUTOSOMAL
; TITLE OF INVENTION: DOMINANT SPASTIC PARAPLEGIA
; FILE REFERENCE: R-341894
; CURRENT APPLICATION NUMBER: US/11/155,492
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: US/09/830,902
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: FR 99 11097
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/FR00/02433
; PRIOR FILING DATE: 2000-09-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 1
; LENGTH: 110000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (9932) ... (10471)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (10472) ... (33718)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (89562) ... (89641)
;
; LOCATION: (33719) ... (33805)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (33806) ... (35748)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (35749) ... (35832)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (35833) ... (45022)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (45023) ... (45118)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (45119) ... (60863)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (60864) ... (61051)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (61052) ... (61927)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (61928) ... (62061)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (62062) ... (62344)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (62345) ... (62438)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (62439) ... (73173)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (73174) ... (73248)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (73249) ... (74633)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (74634) ... (74705)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (74706) ... (82788)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (82789) ... (82864)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (82865) ... (83102)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (83103) ... (83194)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (83195) ... (83334)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (83335) ... (83414)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (83415) ... (88129)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (88130) ... (88172)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (88173) ... (89561)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (89562) ... (89641)
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; FEATURE:
; NAME/KEY: intron
; LOCATION: (89642)...(91162)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (91163)...(91233)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (91234)...(93443)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (93444)...(93484)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (93485)...(100599)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (100600)...(102009)
US-11-155-492-1

Query Match      12.7%  Score 127; DB 7; Length 110000;
Best Local Similarity 81.9%; Pred.No. 3.2e-28;
Matches 163; Conservative 0; Mismatches 25; Indels 11; Gaps 1;

Qy      2  GCTGGGATTACAGGCACCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 61
Db      85942  GATGGGATTACAGGGCGCCACCAACCGCTGGCTTAATTTTGTATTTTAGTAGAGAC 85883

Qy      62  GGGGGTGGGGTGGGGTTTACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGAT 121
Db      85882  G-----GGGTTTACCATTGTTGGTCAGGCTGGTCTCGAACTCCTGACCTCAGGT 85834

Qy      122  GATCACCTGCTCTGCTCTCTTAAGTCTGGGATTACAGGTGTGAGCCACCATGCCAG 181
Db      85833  GATCACCTGCTCTGACCTCTCCAAAGTGTGGGATTACAGGCATGAGCCACTGTGCCAG 85774

Qy      182  CTCAGAAATTTACTCTGTTT 200
Db      85773  CCATTATTTCATTTCTTT 85755
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RESULT 11
US-11-145-703-1/c
; Sequence 1, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilva
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: 53.US16.DIV
; CURRENT APPLICATION NUMBER: US/11/145,703
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US/10/147,603
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 09/539,333
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
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; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 234
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 319608
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31..1107
; OTHER INFORMATION: 5'regulatory region g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1108..1289
; OTHER INFORMATION: exon A g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 14877..14920
; OTHER INFORMATION: exon B g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 18778..18862
; OTHER INFORMATION: exon Bbis g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 25593..25740
; OTHER INFORMATION: exon C g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 29388..29502
; OTHER INFORMATION: exon D g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 29967..30282
; OTHER INFORMATION: exon E g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 64666..64812
; OTHER INFORMATION: exon F g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 65505..65853
; OTHER INFORMATION: exon G g35018 gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 65854..67854
; OTHER INFORMATION: 3'regulatory region g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 94124..94964
; OTHER INFORMATION: exon g35017
; FEATURE:
; NAME/KEY: exon
; LOCATION: 20188..201234
; OTHER INFORMATION: exon S g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 214676..214793
; OTHER INFORMATION: exon T g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 215702..215746
; OTHER INFORMATION: exon U g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 216836..216915
; OTHER INFORMATION: exon V g35030 gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 213818..215818
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OTHER INFORMATION: 3' regulatory region g34872 gene	OTHER INFORMATION: exon Nb1s complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 215819..215941	LOCATION: 215819..215941
OTHER INFORMATION: exon R complement g34872 gene	OTHER INFORMATION: exon R complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 215819..215975	LOCATION: 215819..215975
OTHER INFORMATION: exon Rb1s complement g34872 gene	OTHER INFORMATION: exon Rb1s complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 216661..216952	LOCATION: 216661..216952
OTHER INFORMATION: exon Qb1s complement g34872 gene	OTHER INFORMATION: exon Qb1s complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 216661..217061	LOCATION: 216661..217061
OTHER INFORMATION: exon Q complement g34872 gene	OTHER INFORMATION: exon Q complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 217027..217061	LOCATION: 217027..217061
OTHER INFORMATION: exon Q1 complement g34872 gene	OTHER INFORMATION: exon Q1 complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 229647..229742	LOCATION: 229647..229742
OTHER INFORMATION: exon X complement g34872 gene	OTHER INFORMATION: exon X complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 230408..230721	LOCATION: 230408..230721
OTHER INFORMATION: exon P complement g34872 gene	OTHER INFORMATION: exon P complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 231272..231412	LOCATION: 231272..231412
OTHER INFORMATION: exon Ob1s complement g34872 gene	OTHER INFORMATION: exon Ob1s complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 231787..231880	LOCATION: 231787..231880
OTHER INFORMATION: exon O2 complement g34872 gene	OTHER INFORMATION: exon O2 complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 231870..231879	LOCATION: 231870..231879
OTHER INFORMATION: exon O1 complement g34872 gene	OTHER INFORMATION: exon O1 complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 234174..234321	LOCATION: 234174..234321
OTHER INFORMATION: exon O complement g34872 gene	OTHER INFORMATION: exon O complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 237406..237428	LOCATION: 237406..237428
OTHER INFORMATION: exon Nb1s complement g34872 gene	OTHER INFORMATION: exon Nb1s complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 239719..239807	LOCATION: 239719..239807
OTHER INFORMATION: exon N2 complement g34872 gene	OTHER INFORMATION: exon N2 complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 239719..239853	LOCATION: 239719..239853
OTHER INFORMATION: exon N complement g34872 gene	OTHER INFORMATION: exon N complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 240528..240569	LOCATION: 240528..240569
OTHER INFORMATION: exon M1117 complement g34872 gene	OTHER INFORMATION: exon M1117 complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 240528..240596	LOCATION: 240528..240596
OTHER INFORMATION: exon M1090 complement g34872 gene	OTHER INFORMATION: exon M1090 complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 240528..240617	LOCATION: 240528..240617
OTHER INFORMATION: exon M1069 complement g34872 gene	OTHER INFORMATION: exon M1069 complement g34872 gene
FEATURE:	FEATURE:
NAME/KEY: exon	NAME/KEY: exon
LOCATION: 240528..240644	LOCATION: 240528..240644
OTHER INFORMATION: exon MS2 complement q34872 gene	OTHER INFORMATION: exon MS2 complement q34872 gene

; FEATURE:  
 ; NAME/KEY: exon  
 ; LOCATION: 240528..240824  
 ; OTHER INFORMATION: exon M862 complement g34872 gene  
 ; FEATURE:  
 ; NAME/KEY: exon  
 ; LOCATION: 240528..240994  
 ; OTHER INFORMATION: exon M692 complement g34872 gene  
 ; FEATURE:  
 ; NAME/KEY: exon  
 ; LOCATION: 240528..241685  
 ; OTHER INFORMATION: exon M1 complement g34872 gene  
 ; FEATURE:  
 ; NAME/KEY: exon  
 ; LOCATION: 240800..240993  
 ; OTHER INFORMATION: exon M51 complement g34872 gene  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 241686..243685  
 ; OTHER INFORMATION: 5' regulatory region g34872 gene  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 290652..292652  
 ; OTHER INFORMATION: 3' regulatory region g34665 gene  
 ;  
 Query Match 12.7%; Score 127; DB 7; Length 319608;  
 Best Local Similarity 85.8%; Pred. No. 5.9e-28;  
 Matches 157; Conservative 0; Mismatches 15; Indels 11; Gaps 1;  
 ;  
 QY 2 GCTGGGATTACAGGCACCGCCACCATGCGCCAGCTAAATTTTTTGTATTTTTAGTAGAGAC 61  
 DB 88523 GCTGGGATTACAGGCACCGCCACCATGCGCTGTAGTTTTTGTATTTTTAGTAGAGAC 88464  
 ;  
 QY 62 GGGGGTGGGGTGGGGTTTCCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGAT 121  
 DB 88463 -----TGGGGTTTCACTATGTTAGCCAGGCTGGTCTTGAACCTTCTGATCTCAGGT 88415  
 ;  
 QY 122 GATCCACCTGCGCTCTGCTCTCTAAAGTGTCTGGGATTACAGGTGTGAGCCACCATGCCCCAG 181  
 DB 88414 GATCCACCCACCTCGCGCTCCCAAGAGTCTGGGATTACAGGTGTGAGCCACCATGCCCG 88355  
 ;  
 QY 182 CTC 184  
 DB 88354 CCC 88352  
 ;  
 RESULT 12  
 US-10-995-561-13302  
 ; Sequence 13302, Application US/10995561  
 ; Publication No. US20050272054A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele et al.  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
 ; METHOD OF INVENTION: DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001559  
 ; CURRENT APPLICATION NUMBER: US/10/995,561  
 ; CURRENT FILING DATE: 2004-11-24  
 ; NUMBER OF SEQ ID NOS: 85702  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13302  
 ; LENGTH: 16643  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(16643)  
 ; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see T  
 US-10-995-561-13302  
 ;  
 Query Match 12.6%; Score 126.6; DB 6; Length 16643;  
 Best Local Similarity 86.2%; Pred. No. 1.4e-28;  
 Matches 156; Conservative 0; Mismatches 14; Indels 11; Gaps 1;

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Qy 2 GCTGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 61
Db 932 GCTGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 991
Qy 62 GGGGGTGGGGTGGGGTTACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGAT 121
Db 992 -----AGGGTTTCCCATATTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGGT 1040
Qy 122 GATCCACTGCTCTGCTCTCTAAAGTCTGGGATTACAGGTGAGCCACCATGCCAG 181
Db 1041 GATCCACCGCTCTGGCTCTCCAAAGTCTGGGATTACAGGTGAGCCACCGTGGCCAG 1100
Qy 182 C 182
Db 1101 C 1101

RESULT 13
US-10-995-561-13386
; Sequence 13386, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13386
; LENGTH: 18238
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(18238)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13386

Query Match 12.6%; Score 126.6; DB 6; Length 18238;
Best Local Similarity 86.2%; Pred. No. 1.5e-28;
Matches 156; Conservative 0; Mismatches 14; Indels 11; Gaps 1;

Qy 2 GCTGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 61
Db 8670 GCTGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 8729
Qy 62 GGGGGTGGGGTGGGGTTACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGAT 121
Db 8730 -----AGGGTTTCCCATATTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGGT 8778
Qy 122 GATCCACTGCTCTGCTCTCTAAAGTCTGGGATTACAGGTGAGCCACCATGCCAG 181
Db 8779 GATCCACCGCTCTGGCTCTCCAAAGTCTGGGATTACAGGTGAGCCACCGTGGCCAG 8838
Qy 182 C 182
Db 8839 C 8839

RESULT 14
US-10-995-561-33560
; Sequence 33560, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
```

```
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33560
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-33560

Query Match 12.6%; Score 126.2; DB 6; Length 201;
Best Local Similarity 85.6%; Pred. No. 1.4e-29;
Matches 155; Conservative 1; Mismatches 14; Indels 11; Gaps 1;

Qy 2 GCTGGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 61
Db 32 GCTGGGATTACAGGACCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 91
Qy 62 GGGGGTGGGGTGGGGTTACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGAT 121
Db 92 -----AGGGTTTCCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGGT 140
Qy 122 GATCCACTGCTCTGCTCTCTAAAGTCTGGGATTACAGGTGAGCCACCATGCCAG 181
Db 141 GATCCACTGCTCTGGCTCTCCAAAGTCTAGGATTACAGGTGAGCCACCATGCCAG 200
Qy 182 C 182
Db 201 C 201

RESULT 15
US-11-121-086-18
; Sequence 18, Application US/11121086
; Publication No. US2005026459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 175023
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-18

Query Match 12.6%; Score 125.8; DB 7; Length 175023;
Best Local Similarity 79.4%; Pred. No. 9.9e-28;
Matches 166; Conservative 0; Mismatches 32; Indels 11; Gaps 1;

Qy 2 GCTGGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 61
Db 81959 GCTGGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAT 82018
Qy 62 GGGGGTGGGGTGGGGTTACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGAT 121
Db 82019 G-----GAGTTTCATGTTGGCCAGGCTGGTCTCAAACTCTGACCTCAGGA 82067
Qy 122 GATCCACTGCTCTGCTCTCTAAAGTCTGGGATTACAGGTGAGCCACCATGCCAG 181
Db 82068 GATCCACCCACTCAGCTCTCCAAAGTCTGGGATTACAGGTGAGCCATCATGCCAGG 82127
Qy 182 CTCAGAAATTTACTCTGTTTACGAACATCT 210
Db 82128 CTCAGATCTTAGCTTTATAAATAATATTT 82156
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Search completed: January 10, 2006, 20:45:52  
Job time : 216.333 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 05:49:50 ; Search time 4711 Seconds  
(without alignments)  
9941.386 Million cell updates/sec

Title: US-09-615-039-1\_COPY\_11500\_12500  
Perfect score: 1001  
Sequence: 1 ggctgggattacaggccccc.....gggaccagtggcgtgtggc 1001

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hc:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gse1:\*  
10: gb\_gse2:\*  
11: gb\_gse3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	134.2	13.4	883	5	BQ687748 AGENCOURT
2	133.2	13.3	604	3	BM990713 UI-H-D10-
3	132.6	13.2	1035	3	BM807194 AGENCOURT
4	131.8	13.2	467	9	AQ349390 RPC111-12
5	131.6	13.1	528	7	CN263775 170004241
6	131.2	13.1	723	10	AG030984 Pan ttoq1
7	130.2	13.0	1025	3	BM907570 AGENCOURT
8	129.8	13.0	379	1	AA601673 no01f02.s
9	129.2	12.9	379	1	AI245348 qk28g06.x
10	129.2	12.9	427	1	AW514662 xu97f09.x
11	129.2	12.9	646	1	AW967131 EST379205
12	129	12.9	416	1	AV693536 AV693536
13	129	12.9	421	1	AV691556 AV691556
14	128.8	12.9	488	1	AA720582 rw21h01.s
15	128.8	12.9	603	3	BQ230374 AGENCOURT
16	128.8	12.9	635	2	BE908214 601500472
17	128.8	12.9	657	9	AQ473201 CITBI-B1-
18	128.8	12.9	671	9	AQ470937 CITBI-EI-
19	128.6	12.8	455	9	AQ392348 CITBI-EI-
20	128.6	12.8	490	9	AQ416174 RPC111-1
21	128.4	12.8	536	7	CK821280 i951b10.x
22	128.4	12.8	578	3	BM314487 i951b10.y

23	128.2	12.8	372	3	BM991270
24	128.2	12.8	445	1	AI497824
25	128.2	12.8	674	5	EX501315
26	128.2	12.8	854	6	CD171905
27	128	12.8	894	5	BQ439884
28	128	12.8	1840	4	CR857550
29	127.4	12.7	417	1	AV697609
30	127.4	12.7	571	9	AQ381323
31	127.2	12.7	633	3	BM977586
32	127.2	12.7	430	9	AQ393433
33	126.6	12.6	361	9	AQ014345
34	126.6	12.6	601	7	CR549909
35	126.6	12.6	635	7	CN265093
36	126.6	12.6	660	9	AQ014266
37	126.6	12.6	767	5	BQ775984
38	126.6	12.6	1808	4	AF130050
39	126.6	12.6	2110	4	BC012538
40	126.4	12.6	288	9	AQ391637
41	126.4	12.6	392	1	AA484892
42	126.4	12.6	436	2	BF816190
43	126.4	12.6	437	1	AA572921
44	126.4	12.6	689	10	AG146015
45	126.2	12.6	311	6	CB230206

#### ALIGNMENTS

RESULT 1  
BQ687748

LOCUS

DEFINITION

AGENCOURT 8186578 NIH\_MGC\_110 Homo sapiens

5', mRNA sequence.

ACCESSION

BQ687748

VERSION

BQ687748.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1 (bases 1 to 883)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgsapb@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Sequencing by: The I.M.A.G.E. Consortium (ILNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILNL at:

http://image.llnl.gov

Plate: LLCM2396 row: f column: 20

High quality sequence stop: 531.

Location/Qualifiers

1..883

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6251539"

/tissue\_type="ductal carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_110"

/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 13.4%; Score 134.2; DB 5; Length 883;  
 Best Local Similarity 81.5%; Pred. No. 2.4e-19;  
 Matches 172; Conservative 0; Mismatches 28; Indels 11; Gaps 1;  
 QY 2 GCTGGGATTACAGCAGCCGCCACCATGTCGCCAGCTGTCTCGAATTTCTGATTTTGTAGAGAC 61  
 DB 237 GCTGGGATCAGGAGCAGCTGCCACATGTCGCCAGCTGTCTCAACACCTGACCTCAAT 296  
 QY 62 GGGGGTGGGGTGGGGTTTCCATCTTTGGCCAGCTGTCTCGAATTTCTGATTTTGTAGAGAC 121  
 DB 297 A-----GGGTTTCCATGTTGGCCAGCTGTCTCAACACCTGACCTCAAT 345  
 QY 122 GATCACCTGCTCTGCTCTCTAAAGTCTGGGATTACAGTGTGAGCCACCATGCCAG 181  
 DB 346 GATCACCTGCTCAGCTCTCCAAAGTGTGGGATTACAGGCGTAAGCCACCATGCCAG 405  
 QY 182 CTCAGATTACTCTGTTTAAACATCTGG 212  
 DB 406 CCCTGAATTAATAATTTTAAATAAGTTGG 436

## RESULT 2

BM990713  
 LOCUS  
 DEFINITION UI-H-D10-atr-m-07-0-UI.s1 NCI CGAP D10 Homo sapiens cDNA clone  
 IMAGE:5863470 3', mRNA sequence.

ACCESSION  
 BM990713

VERSION  
 BM990713.1 GI:19710102

KEYWORDS  
 EST.

SOURCE  
 Homo sapiens (human)

ORGANISM  
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

1 (bases 1 to 604)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Dr. Jose Mercuende

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

The following repetitive elements were found in this cDNA

sequence: 11-302, >ALU (matched complement) 218-325, >ALU (matched

complement)

Seq primer: M13 FORWARD

POLYA=Yes.

## FEATURES

source

Location/Qualifiers

1..604

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5863470"

/tissue\_type="Lung Focal Fibrosis"

/dev\_stage="Adult"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI CGAP D10"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI CGAP D10 is a cDNA library containing the following

tissues): A pool of Lung Focal Fibrosis. The library was

constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dT primer containing a

Not I site. Double stranded cDNA was ligated to an EcoR I

adaptor, digested with Not I, and cloned directionally

into pT7T3-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (drr)18 tail. The sequence tag for this library is  
 ATACGGGCTC.

TAG TISSUE=lung with fibrosis

TAG LIB=UI-H-D10

TAG SEQ=ATACGGGCTC"

## ORIGIN

Query Match 13.3%; Score 133.2; DB 3; Length 604;  
 Best Local Similarity 74.4%; Pred. No. 4e-19;  
 Matches 186; Conservative 0; Mismatches 53; Indels 11; Gaps 1;

QY 2 GCTGGGATTACAGCAGCCGCCACCATGTCGCCAGCTGTCTCGAATTTCTGATTTTGTAGAGAC 61

DB 132 GCTGGGATTACAGCAGCCGCCACCATGTCGCCAGCTGTCTCGAATTTCTGATTTTGTAGAGAT 191

QY 62 GGGGGTGGGGTGGGGTTTCCATGTTGGCCAGCTGTCTCGAATTTCTGACCTCAGAT 121

DB 192 G-----GGGTTTCCATGTTGGCCAGCTGTCTCGAATTTCTGACCTCAGGT 240

QY 122 GATCCACCTGCTCTGCTCTCTAAAGTCTGGGATTACAGTGTGAGCCACCATGCCAG 181

DB 241 GATCCGCCGCTCTGGGCTCTCCAAAGTCTGGGATTACAGGCGTGAAGCCAGCCGCCAG 300

QY 182 CTGAGAAATTTACTCTCTGTTTAAACATCTGGGCTCTGAGGTAGGAAGCTCAACCCACCTCNA 241

DB 301 CCAACCTTACTACTATTTTAAAGAAATTTTCCAGAGTTTAAATTTCTGACATAGCTTAA 360

QY 242 GTGTTGTGGT 251

DB 361 GTTTCAGT 370

## RESULT 3

BM807194/c

LOCUS

DEFINITION

BM807194

VERSION

BM807194.1

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1035)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM12749 row: k column: 12

High quality sequence stop: 675.

Location/Qualifiers

1..1035

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5738243"

/tissue\_type="duodenal

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 88"

/note="Organ: small intestine; Vector: pCMV-SPORT6;

Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

```

ORIGIN
Query Match      13.2%; Score 132.6; DB 3; Length 1035;
Best Local Similarity 79.5%; Pred. No. 5.4e-19;
Matches 174; Conservative 0; Mismatches 34; Indels 11; Gaps 1;

Qy 2 GCTGGGATTACAGGACCCGCCACATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 61
    |||||
Db 489 GCTGGGATTACAGGACATCGCCACATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 430
    |||||

Qy 62 GGGGGTGGGGTGGGTTCCACATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGAT 121
    |||||
Db 429 G-----GGGTTTCACATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGGT 381
    |||||

Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCAG 181
    |||||
Db 380 GATCCACAGCTCGGCTCTCCAAGTCTGGGATTACAGGTGTGAGCCACCATGCTGCG 321
    |||||

Qy 182 CTCAGAAATTACTCTGTTTAGAAACATCTGGGTCTGAGG 220
    |||||
Db 320 CCCAAACTATTTTAAAGATATAAAATGCTCACAG 282
    |||||

```

```

RESULT 4
LOCUS      AQ349390
DEFINITION RPC111-120M7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-120M7,
            genomic survey sequence.
ACCESSION  AQ349390
VERSION     AQ349390.1 GI:4174286
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1 (bases 1 to 467)
            Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
            Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
            Unpublished (1997)
            Other GSSs: RPC111-120M7.TV
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genetics (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
            Seq primer: SP6
            Class: BAC ends.
            Location/Qualifiers
                1..467
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="GDB:754590"
                /db_xref="taxon:9606"
                /clone="RPCI-11-120M7"
                /sex="Male"
                /cell_type="Lymphocytes"
                /clone_lib="RPCI-11"
                /note="Vector: pBACe3.6; Site.1: EcoRI; Site.2: EcoRI;

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```

FEATURES
            source
                1..467
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /tissue_type="embryonic stem cells, embryoid bodies
                derived from H1, H7 and H9 cells"
                /clone_lib="GRN_EB"
                /note="Oligo dT primed, full-length enriched cDNA library
                from embryoid body outgrowths derived from hES cell lines
                H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                conditions."

```

```

ORIGIN
Query Match      13.2%; Score 131.8; DB 9; Length 467;
Best Local Similarity 83.4%; Pred. No. 8.2e-19;
Matches 166; Conservative 0; Mismatches 22; Indels 11; Gaps 1;

Qy 2 GCTGGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 61
    |||||
Db 261 GCTGGGATTACAGGACCTCGCCACCATGTCAGCTAAATTTTGTATTTTAGTAGAGAC 320
    |||||

Qy 62 GGGGGTGGGGTGGGTTTCACATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGAT 121
    |||||
Db 321 G-----GGGTTTCACATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGGT 369
    |||||

Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCAG 181
    |||||
Db 370 GATCCACCTGCTCGGCTCTCCAAGTCTGGGATTACAGGTGTGAGCCACCATGCCAG 429
    |||||

Qy 182 CTCAGAAATTACTCTGCTTT 200
    |||||
Db 430 CCTATTTATTTATTTT 448
    |||||

```

```

RESULT 5
LOCUS      CN263775
DEFINITION 17000424180545 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION  CN263775
VERSION     CN263775.1 GI:47280189
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1 (bases 1 to 528)
            Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Pang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowek,J and Stanton,L.W.
            Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
            Nat. Biotechnol. 22 (6), 707-716 (2004)
            15146197
            Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 528 Std Error: 0.00.
            Location/Qualifiers
                1..528
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /tissue_type="embryonic stem cells, embryoid bodies
                derived from H1, H7 and H9 cells"
                /clone_lib="GRN_EB"
                /note="Oligo dT primed, full-length enriched cDNA library
                from embryoid body outgrowths derived from hES cell lines
                H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                conditions."

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```

FEATURES
            source
                1..528
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /tissue_type="embryonic stem cells, embryoid bodies
                derived from H1, H7 and H9 cells"
                /clone_lib="GRN_EB"
                /note="Oligo dT primed, full-length enriched cDNA library
                from embryoid body outgrowths derived from hES cell lines
                H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                conditions."

```

```

ORIGIN
Query Match      13.1%; Score 131.6; DB 7; Length 528;
Best Local Similarity 81.0%; Pred. No. 9.1e-19;
Matches 170; Conservative 0; Mismatches 29; Indels 11; Gaps 1;

Qy 2 GCTGGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 61
    |||||
Db 166 GCTGGGATTACAGGTGGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 225
    |||||

```

```

Qy 62 GGGGGTGGGGTTCACCATGTTGGCAGGCTGGTCTCGAATCTTCTGACCTCAGAT 121
Db |-----|-----|-----|-----|-----|-----|-----|-----|
226 G-----|-----|-----|-----|-----|-----|-----|-----|
Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTAACAGTGTGAGCCACCATGCCCGAG 181
Db |-----|-----|-----|-----|-----|-----|-----|-----|
275 GATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTAACAGTGTGAGCCACCATGCCCGAG 334
Qy 182 CTGAGAAATTTACTCTGTTTGAACATCTG 211
Db |-----|-----|-----|-----|-----|-----|-----|-----|
335 CCCTGTGCTTACTCTTAATGAATTTTGTG 364

RESULT 6
AG030984/c
LOCUS
DEFINITION Pan troglodytes DNA, clone: PTB-003114.R, genomic survey sequence.
ACCESSION AG030984
VERSION AG030984.1 GI:16557857
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
REFERENCE
1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 723)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanzee@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
FEATURES
Location/Qualifiers
source 1..723
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-003114.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match 13.1%; Score 131.2; DB 10; Length 723;
Best Local Similarity 81.2%; Pred. No. 1.1e-18;
Matches 169; Conservative 0; Mismatches 28; Indels 11; Gaps 1;

Qy 2 GCTGGGATTAACAGCACCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGAC 61
Db |-----|-----|-----|-----|-----|-----|-----|-----|
437 GCTGGGATTAACAGTGCCCGCCATCACACCATCAATTTTGTATTTTGTAGTAGAGAC 378

Qy 62 GGGGGTGGGGTTCACCATGTTGGCAGGCTGGTCTCGAATCTTCTGACCTCAGAT 121
Db |-----|-----|-----|-----|-----|-----|-----|-----|
377 G-----|-----|-----|-----|-----|-----|-----|-----|

Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTAACAGTGTGAGCCACCATGCCCGAG 181
Db |-----|-----|-----|-----|-----|-----|-----|-----|
329 CCCTGTGCTTACTCTTAATGAATTTTGTG 364

Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTAACAGTGTGAGCCACCATGCCCGAG 181
Db |-----|-----|-----|-----|-----|-----|-----|-----|
329 CCCTGTGCTTACTCTTAATGAATTTTGTG 364

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Db 328 GATCCACCTGCTCTGACCTCCCAAGTGTGGGATTAACAGTGTGAGCCACCATGCCCGAG 269
Qy 182 CTGAGAAATTTACTCTGTTTGAACATC 209
Db 268 CCTGAAATCTGCACCTTTTGACAAGCATC 241

RESULT 7
BM907570/c
LOCUS
DEFINITION BM907570 1025 bp mRNA linear EST 12-MAR-2002
5', mRNA sequence.
ACCESSION BM907570
VERSION BM907570.1 GI:19357949
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 1025)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: DCTP/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12743 row: h column: 21
High quality sequence stop: 606.
FEATURES
Location/Qualifiers
source 1..1025
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5735876"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 13.0%; Score 130.2; DB 3; Length 1025;
Best Local Similarity 81.2%; Pred. No. 1.9e-18;
Matches 168; Conservative 0; Mismatches 28; Indels 11; Gaps 1;

Qy 2 GCTGGGATTAACAGCACCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGAC 61
Db 429 GCTGGGACTACAGCGCCACCATACCTGGCTAAATTTTGTATTTTGTAGTAGAGAC 370

Qy 62 GGGGGTGGGGTTCACCATGTTGGCAGGCTGGTCTCGAATCTTCTGACCTCAGAT 121
Db 369 AGGGT-----TTATCCATGTTGGCCAGGCTGGTCTCAACTCTGACCTCAAGT 321

Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTAACAGTGTGAGCCACCATGCCCGAG 181
Db 320 GATCTCTCTGCTCGGCTCCCAAGTGTGGGATTAACAGTGTGAGCCACCATGCCCGAG 261

Qy 182 CTGAGAAATTTACTCTGTTTGAACAT 208
Db 260 CCAATAATTTCTTGATATAATAAAT 234

RESULT 8

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AA601673/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source	ORIGIN
AA601673	nc01102.81	NCI_CGAP Phel Homo sapiens cDNA clone IMAGE:1099419 3', similar to contains Alu repetitive element;, mRNA sequence.	AA601673	AA601673.1	GI:2435298	Homo sapiens (human)	Homo sapiens	1 (bases 1 to 379)	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	Unpublished (1997)	Contact: Robert Strausberg, Ph.D. Email: rcgape@remail.nih.gov Tissue Procurement: W. Marston Linehan, M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Stratagene, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1018 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 373.	1. 379 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:1099419" /tissue_type="pheochromocytoma" /lab_host="SOLR (kanamycin resistant)" /clone_lib="NCI_CGAP_Phel" /note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dr. Pheochromocytoma. 5' adaptor sequence: 5' GAATTCGGCAGG 3' 3' adaptor sequence: 5' CTCGAGTGTGTGTGTGTGTGTGTGT 3' Average insert size: 1.3 kb."	Query Match 13.0%; Score 129.8; DB 1; Length 379; Best Local Similarity 69.1%; Pred. No. 2.3e-18; Matches 197; Conservative 0; Mismatches 77; Indels 11; Gaps 1;  2 GCTGGGATTACAGGCACCGCCACCATCGCCAGCTAAATTTTGTATTTTAGTAGAGAC 61 374 GCTGGGATTACAGGCACCGCCACCATCGCCAGCTAAATTTTGTATTTTAGTAGAGAC 315  62 GGGGGTGGGGTGGGGTTTACCATTGTGGCCAGGCTGCTCTCGAACTTCTGACCTCAGAT 121 314 -----AGGGTTTCGCCATGTGTGGCCAGTGTGCTCTCGAACTCTGACCTCAGGA 266  122 GATCCACTGCGCTCTGCGCTCTTAAGTGTCTGGGATTACAGGTGTGAGCCACCATGCCGAG 181 265 GATCCACCTGCTTTCAGCTTCCCAAGTGTGGGATTACAGGCGTGAGCCACCGCGCCGAG 206  182 CTCAGAAATTACTCTGTTTTAGAAAACATCTGGGTCTGAGGTAGGAAGCTCAGCCCACTCAA 241 205 CCTACAGCCTAATCTATATGTGTCTCAATGCTGTAGGTGTCTCATTTGTTTCTAGGCT 146  242 GTGTTGTGGTGTGTTTAAGCCCAATGATAGAAATTTTTTTTATGTGTT 286 145 TTTTCAGTCAAGAGCTTAAAGAGCTAGAAAAACACACTTTTTTTTTTT 101 Db Db

RESULT 9  
AI245348

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LOCUS           AI245348             379 bp      mRNA          linear      EST 28-JAN-1999
DEFINITION      qx28906.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1870330 3'
                 similar to contains Alu repetitive element; , mRNA sequence.
ACCESSION       AI245348
VERSION         AI245348.1
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE       1. (bases 1 to 379)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
JOURNAL         Unpublished (1997)
COMMENT        Contact: Robert Straubeberg, Ph.D.
               Email: csagbs-x@mail.nih.gov
               Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
               Emmert-Buck, M.D., Ph.D.
               cDNA Library Preparation: M. Bento Soares, Ph.D.
               cDNA Library Arrayed by: Greg Lennon, Ph.D.
               DNA sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html
               Insert length: 559 Std Error: 0.00
               Seq primer: -40UP from Gibco
               High quality sequence stop: 364.
FEATURES             Location/Qualifiers
                     1. .379
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:1870330"
                        /lab_host="DH10B"
                        /clone_lib="NCI_CGAP_Kid3"
                        /notes="Organ: kidney; Vector: pTTT3D-Pac (Pharmacia) with
                        a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
                        strand cDNA was primed with a Not I - oligo(dT) primer,
                        double-stranded cDNA was ligated to Eco RI adaptors
                        (Pharmacia), digested with Not I and cloned into the Not
                        I and Eco RI sites of the modified pT73 vector. mRNA
                        source: 2 pooled kidneys. Library went through one round
                        of normalization. Library constructed by Bento Soares and
                        M. Fatima Bonaldo. "
ORIGIN
Query Match      12.9%; Score 129.2; DB 1; Length 379;
Best Local Similarity 86.8%; Pred. No. 3.1e-18;
Matches 158; Conservative 0; Mismatches 13; Indels 11; Gaps 1;

QY 1  GGCTGGGATTACAGGCACCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 60
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DB 116 GGCTGGGATTACAGGCATGCGCCACCATGCCCGGCTAATTTTGTATTTTGTATTTATAGAGA 175
    |||
QY 61  CGGGGGTGGGGGTTCCAGCATGTTGGCCAGCGTGGTCTCGAACTCTTGACCTCAGA 120
    |||
DB 176 CG-----GGGTTTCAACATGTTGCCAGCGTGCCTCGAATCTTCGACCTCAGG 224
    |||
QY 121 TGATCCACCTGCCTCTGCCTCTTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCCA 180
    |||
DB 225 TGGTCCACCTGCCTCAGCCTCCGAAGGTGCTGGGATTACAGGCGTGAGCCACCATGCCCCA 284
    |||
QY 181 GC 182
    ||
DB 285 GC 286

RESULT 10
AWS14662/c      AWS14662
LOCUS           xu97f09.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2809673 3'
DEFINITION

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PRINCE-T 10

AW514662/C

STUDY LOCUS

## DEFINITION

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similar to contains Alu repetitive element, mRNA sequence.

AW514662  
 VERSION AW514662.1 GI:7152744  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 427)  
 REFERENCE NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: Greg Lennon, Ph.D.  
 Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: [image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 399.

FEATURES  
 source Location/Qualifiers  
 1..427  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2809673"  
 /tissue\_types="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut2"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 Kb. Life Technologies catalog #: 11539-012"

Query Match 12.9%; Score 129.2; DB 1; Length 427;  
 Best Local Similarity 81.1%; Pred. No. 3.1e-18;  
 Matches 167; Conservative 0; Mismatches 28; Indels 11; Gaps 1;

Qy 2 GCTGGGATTACAGCACCCGCCACCATGCCAGCTAATTTTTTGTATTTTAGTAGAGAC 61  
 |||||  
 Db 215 GCTGGGACTACAGCACCCGCCACCATGCCAGCTAATTTTTTGTATTTTAGTAGAGAT 156  
 |||||

Qy 62 GGGGGTGGGGTGGGGTTACCATGTTGGCCAGGCTGGTCTCGAATCTTCGACCTCAGAT 121  
 |||||  
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Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTCTGGGATTACAGTGTGACCCACCATGCCCG 181  
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 Db 106 GATCCACCGCTCAGCTCTCCAAAGTCTGGGATTACAGTGTGAGGACCAACACCCCG 47  
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Qy 182 CTCAGAAATTTACTCTGTTTGAACA 207  
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 ACCESSION AW967131  
 VERSION AW967131.1 GI:8156967  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 646)  
 REFERENCE Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,  
 AUTHORS Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.  
 TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: John Quackenbush  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 3528  
 Fax: 301 838 0208  
 Email: johnq@tigr.org  
 Plate: 237  
 Seq primer: Reverse.  
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Qy 62 GGGGGTGGGGTGGGGTTACCATGTTGGCAGGCTGGTCTCGAATCTTCGACCTCAGAT 121  
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Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTCTGGGATTACAGTGTGAGGACCAACATGCCCG 181  
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Qy 182 CTCAGAAATTT 191  
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 LOCUS  
 DEFINITION AV693536 GKC Homo sapiens cDNA clone GKCCQF10 5', mRNA sequence.  
 ACCESSION AV693536  
 VERSION AV693536.1 GI:10295399  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 416)  
 REFERENCE Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,  
 AUTHORS Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.  
 TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)  
 PUBMED 11752456  
 COMMENT Contact: Zeguang Han  
 Chinese National Human Genome Center at Shanghai  
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China

Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at

**FEATURES**  
**source**

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	DEFINITION	AV691556	GKC Homo sapiens cDNA clone GRCPCPH1	5'	mRNA sequence.	

REFERENCE

1. (Pages 1 to 421)

AUTHORS

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.

TITLE

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

PUBMED

11752456

## FEATURES

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Qy	122	GATCCACCTGCCTCTGCCTCTTAAGTGTCTGGGANTTACAGGTGTGAGCCACCATGCCCAG	181	
Db	241	GATCCACCGGCTCAGGCTCCCAAGTGTCTGGGANTTACAGGCAGGAGCCACCAAGCCCG	300	
Qy	182	CTCAGAATTTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCACTCAA	241	
Db	301	CCTAACAATTTTATCTTTACCAAGAAATTCCTCAAGAGACCCCTGGTGTGCCACAAATGCAA	360	
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RESULT 14  
AA720582

ACCESSION  
VERSION  
KEYWORDS

## REFERENCE

## FEATURES





GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 10:27:39 ; Search time 205 Seconds  
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

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Listing first 45 summaries

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- 9: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	1001	100.0	15418	3	US-09-783-203-1
3	1001	100.0	15418	3	US-09-994-427A-1
4	1001	100.0	15418	3	US-09-244-438-1
5	1001	100.0	15418	3	US-09-995-419A-1
6	1001	100.0	44952	3	US-09-949-016-12197
7	1001	100.0	44960	3	US-09-949-016-17583
8	972.8	97.2	51552	3	US-09-733-294A-30
9	930.8	93.0	4335	3	US-08-974-549A-6
10	930.8	93.0	4335	3	US-09-721-456-6
11	677.8	67.7	35871	3	US-09-956-335-2
12	677.8	67.7	35978	3	US-09-956-335-1
13	676	67.5	1677	3	US-09-956-335-3
14	497	49.7	497	3	US-09-244-438-22
15	229.8	23.0	4200	3	US-08-912-931-6
16	134.2	13.4	18596	3	US-09-318-448-11
17	134.2	13.4	18596	3	US-09-577-266-11
18	134.2	13.4	18597	3	US-09-962-665-8
19	134.2	13.4	18597	3	US-09-963-333-8
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28	131.8	13.2	3129	3	US-10-045-428A-9	Sequence 9, Appli
29	131.8	13.2	137949	3	US-09-949-016-12196	Sequence 12196, A
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33	131.6	13.1	140982	3	US-09-949-016-16295	Sequence 16295, A
34	131.4	13.1	140982	3	US-09-949-016-66371	Sequence 66371, A
c 35	131.2	13.1	60304	3	US-09-949-016-12218	Sequence 12218, A
c 36	131.2	13.1	60305	3	US-09-949-016-15791	Sequence 15791, A
37	131	13.1	121982	3	US-09-949-016-12085	Sequence 12085, A
38	131	13.1	121982	3	US-09-949-016-14105	Sequence 14105, A
39	130.2	13.0	91831	3	US-09-949-016-13694	Sequence 13694, A
40	129.8	13.0	601	3	US-09-949-016-66372	Sequence 66372, A
c 41	129.8	13.0	129554	3	US-09-949-002-765	Sequence 765, App
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## ALIGNMENTS

### RESULT 1

US-09-402-181B-6  
; Sequence 6, Application US/09402181B  
; Patent No. 6610839  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 633  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09402,181B  
; FILING DATE: 29-Sep-1997  
; CLASSIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4321 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
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; Patent No. 6576464  
; GENERAL INFORMATION:  
; APPLICANT: Geron Corporation  
; APPLICANT: Gold, Joseph  
; APPLICANT: Lebkowski, Jane  
; TITLE OF INVENTION: Tpacked stem cells  
; FILE REFERENCE: 096/003  
; CURRENT APPLICATION NUMBER: US/09/783,203  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: 60/253,443  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/253,357  
; PRIOR FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 7  
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; SEQ ID NO 1  
; LENGTH: 15418  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-783-203-1

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Qy 661 ACCGTAATCTTAAGTATTTAAAGAGGCTTAGGGATCACTAAGGGATTTCTAGAGAGCG 720  
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Qy 721 GAGGTGCGAGCCCTGTTCAAATGCTAGCTCCATAAATAAAGCAATTTCTCCGGCAGTT 780  
Db 12220 GAGGTGCGAGCCCTGTTCAAATGCTAGCTCCATAAATAAAGCAATTTCTCCGGCAGTT 12279  
Qy 781 TCTGAAAGTAGGAAGGTTTCAATTAAGTTGCGTTTGTAGCATTTTCAAGTGTTCGGA 840  
Db 12280 TCTGAAAGTAGGAAGGTTTCAATTAAGTTGCGTTTGTAGCATTTTCAAGTGTTCGGA 12339  
Qy 841 CCTCAGCTACAGCATCCCTGCAAGCCCTCGGAGACCCAGAAAGTTTCTCGCCCTTAGAT 900  
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Qy 901 CCAAACTTGAGCAACCCGGAGTCTGGATTCTGGGAAGTCTCTCAGCTGCTCCTGGGTTGT 960  
Db 12400 CCAAACTTGAGCAACCCGGAGTCTGGATTCTGGGAAGTCTCTCAGCTGCTCCTGGGTTGT 12459  
Qy 961 GCCGGGGCCCGAGTCTGGAGGGACCAAGTGGCCGTGTGGC 1001  
Db 12460 GCCGGGGCCCGAGTCTGGAGGGACCAAGTGGCCGTGTGGC 12500

RESULT 3

US-09-994-427A-1  
; Sequence 1, Application US/09994427A  
; Patent No. 6713055  
; GENERAL INFORMATION:  
; APPLICANT: Genon Corporation  
; APPLICANT: Schliff, J. Michael  
; TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER  
; FILE REFERENCE: 083,002  
; CURRENT APPLICATION NUMBER: US/09/994,427A  
; CURRENT FILING DATE: 2002-02-26  
; PRIOR APPLICATION NUMBER: 60/253,395  
; PRIOR FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 15418  
; TYPE: DNA

; ORGANISM: Homo sapiens  
US-09-994-427A-1  
Query Match 100.0%; Score 1001; DB 3; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 2.1e-287; Indels 0; Gaps 0;  
Matches 1001; Conservative 0; Mismatches 0;  
Qy 1 GGCCTGGGATTTACAGGACCCCGCCACCATGCCCAGTAAATTTTGTATTTTGTAGTAGAGA 60  
Db 11500 GGCCTGGGATTTACAGGACCCCGCCACCATGCCCAGTAAATTTTGTATTTTGTAGTAGAGA 11559  
Qy 61 CGGGGGTGGGGGTGGGGTTTCAATGTTGGCAGGCTGGTCTCGAATCTTCTGACTCTAGA 120  
Db 11560 CGGGGGTGGGGGTGGGGTTTCAATGTTGGCAGGCTGGTCTCGAATCTTCTGACTCTAGA 11619  
Qy 121 TGATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTTACAGGTGTGAGCCACCAATGCCCA 180  
Db 11620 TGATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTTACAGGTGTGAGCCACCAATGCCCA 11679  
Qy 181 GCTCAGAAATTTACTCTCTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240  
Db 11680 GCTCAGAAATTTACTCTCTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 11739  
Qy 241 AGTGTCTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTGTTGTTAGAACACTCTTGA 300  
Db 11740 AGTGTCTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTGTTGTTAGAACACTCTTGA 11799  
Qy 301 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGACACC 360  
Db 11800 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGACACC 11859  
Qy 361 ATAATACCTGGGTGTCTTCTGGGTATCAGCGATCTTCAATGGAATCCGGGAGGGGTTTC 420  
Db 11860 ATAATACCTGGGTGTCTTCTGGGTATCAGCGATCTTCAATGGAATCCGGGAGGGGTTTC 11919  
Qy 421 TCGCCATGCAATGTTTAAATTAATCTCCAGCATATCTTCTGCTTCCATTTCTCTCTTC 480  
Db 11920 TCGCCATGCAATGTTTAAATTAATCTCCAGCATATCTTCTGCTTCCATTTCTCTCTTC 11979  
Qy 481 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGCAGAGAACAGTGTAAAGTACA 540  
Db 11980 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGCAGAGAACAGTGTAAAGTACA 12039  
Qy 541 ACTTAACTTTTGGAAACAAATTTTCAAACCCGCCCTTTGCCCTAGTGGCAGACAA 600  
Db 12040 ACTTAACTTTTGGAAACAAATTTTCAAACCCGCCCTTTGCCCTAGTGGCAGACAA 12099  
Qy 601 TTCAAAACACAGCCCTTTAAAGGCTTAGGGATCACTAAGGGATTTCTAGAGAGCG 660  
Db 12100 TTCAAAACACAGCCCTTTAAAGGCTTAGGGATCACTAAGGGATTTCTAGAGAGCG 12159  
Qy 661 ACCGTAATCTTAAGTATTTAAAGAGGCTTAGGGATCACTAAGGGATTTCTAGAGAGCG 720  
Db 12160 ACCGTAATCTTAAGTATTTAAAGAGGCTTAGGGATCACTAAGGGATTTCTAGAGAGCG 12219  
Qy 721 GAGGTGCGAGCCCTGTTCAAATGCTAGCTCCATAAATAAAGCAATTTCTCCGGCAGTT 780  
Db 12220 GAGGTGCGAGCCCTGTTCAAATGCTAGCTCCATAAATAAAGCAATTTCTCCGGCAGTT 12279  
Qy 781 TCTGAAAGTAGGAAGGTTTCAATTAAGTTGCGTTTGTAGCATTTTCAAGTGTTCGGA 840  
Db 12280 TCTGAAAGTAGGAAGGTTTCAATTAAGTTGCGTTTGTAGCATTTTCAAGTGTTCGGA 12339  
Qy 841 CCTCAGCTACAGCATCCCTGCAAGCCCTCGGAGACCCAGAAAGTTTCTCGCCCTTAGAT 900  
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Qy 901 CCAAACTTGAGCAACCCGGAGTCTGGATTCTGGGAAGTCTCTCAGCTGCTCCTGGGTTGT 960  
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RESULT 4
US-09-244-438-1
; Sequence 1, Application US/09244438
; Patent No. 677203
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; FILE OF INVENTION: Regulatory Sequences and Methods of Using
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/09/244,438
; CURRENT FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-09-244-438-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 2.1e-287;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGTGGGATTTACAGGACCCCGCCACCATGCGCCAGTAAATTTTGTATTTTGTAGTAGAGA 60
Db 11500 GCGTGGGATTTACAGGACCCCGCCACCATGCGCCAGTAAATTTTGTATTTTGTAGTAGAGA 11559

Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGAGGTGCTCGAGCTTCTCGAATCTTGACCTCAGA 120
Db 11560 CGGGGGTGGGGTGGGGTTCACCATGTTGGAGGTGCTCGAGCTTCTCGAATCTTGACCTCAGA 11619

Qy 121 TGAATCCACTGTCCTCTCCCTCTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCCA 180
Db 11620 TGAATCCACTGTCCTCTCCCTCTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCCA 11679

Qy 181 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGGCTCAGGTAGGAAGCTCACCCCACTCA 240
Db 11680 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGGCTCAGGTAGGAAGCTCACCCCACTCA 11739

Qy 241 AGTGTGTGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTGTAGAACACTCTTGA 300
Db 11740 AGTGTGTGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTGTAGAACACTCTTGA 11799

Qy 301 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAATGCAACCC 360
Db 11800 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAATGCAACCC 11859

Qy 361 ATAATACCTGGGGTCTCTTCTGGGTATCAGGATCTTCAATGAATCCGGGAGGGGTTTCC 420
Db 11860 ATAATACCTGGGGTCTCTTCTGGGTATCAGGATCTTCAATGAATCCGGGAGGGGTTTCC 11919

Qy 421 TCGCCATGCACATGGTGTAAATTAATCTCCAGCATAACTCTGCTTCCATTTCTTCTCTTC 480
Db 11920 TCGCCATGCACATGGTGTAAATTAATCTCCAGCATAACTCTGCTTCCATTTCTTCTCTTC 11979

Qy 481 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGTAGCTTACA 540
Db 11980 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGTAGCTTACA 12039

Qy 541 ACTTAATCTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGGCTAGTGGCAGAGACAA 600
Db 12040 ACTTAATCTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGGCTAGTGGCAGAGACAA 12099

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Db 12160 ACCCGTAATCTTAAGTATTTTACAAGACGAGGCTTAACCTCCAGCGAGCGTGCACAGCCAGG 12219

Qy 721 GAGGTGCGAGGCGCTGTTCAATGCTAGCTTCAATAATAAGCAATTTCTCCGGCAGTT 780
Db 12220 GAGGTGCGAGGCGCTGTTCAATGCTAGCTTCAATAATAAGCAATTTCTCCGGCAGTT 12279

Qy 781 TCTGAAAGTAGGAAAGCTTACATTTAAGGTTGGGTTTGTAGCAATTTCACTGTTTGGCGGA 840
Db 12280 TCTGAAAGTAGGAAAGCTTACATTTAAGGTTGGGTTTGTAGCAATTTCACTGTTTGGCGGA 12339

Qy 841 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAAAGTTTCTCCGCCCTTAGAT 900
Db 12340 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAAAGTTTCTCCGCCCTTAGAT 12399

Qy 901 CCAAACTTGAGCAACCCGGAGTCTGGATTTCTTGGGAGTCTCAGCTGTCTCGGGTGT 960
Db 12400 CCAAACTTGAGCAACCCGGAGTCTGGATTTCTTGGGAGTCTCAGCTGTCTCGGGTGT 12459

Qy 961 GCCGGGGCCCCAGGCTCTGGAGGGGACCCAGTGGCGCTGTGGC 1001
Db 12460 GCCGGGGCCCCAGGCTCTGGAGGGGACCCAGTGGCGCTGTGGC 12500

RESULT 5
US-09-995-419A-1
; Sequence 1, Application US/09995419A
; Patent No. 6921665
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: McWhir, Jim
; APPLICANT: Gold, Joseph D.
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: 096,004 - SeqList
; FILE REFERENCE: 096,004 - SeqList
; CURRENT APPLICATION NUMBER: US/09/995,419A
; PRIOR FILING DATE: 2001-11-26
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-995-419A-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 2.1e-287;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGTGGGATTTACAGGACCCCGCCACCATGCGCCAGTAAATTTTGTATTTTGTAGTAGAGA 60
Db 11500 GCGTGGGATTTACAGGACCCCGCCACCATGCGCCAGTAAATTTTGTATTTTGTAGTAGAGA 11559

Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA 120
Db 11560 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA 11619

Qy 121 TGAATCCACTGTCCTCTCCCTCTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCCA 180
Db 11620 TGAATCCACTGTCCTCTCCCTCTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCCA 11679

Qy 181 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGGCTCAGGTAGGAAGCTCACCCCACTCA 240
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Qy 301 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAATGCAACCC 360
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Qy 361 ATAATACCTGGGGTCTCTTCTGGGTATCAGGATCTTCAATGAATCCGGGAGGGGTTTCC 420
Db 11860 ATAATACCTGGGGTCTCTTCTGGGTATCAGGATCTTCAATGAATCCGGGAGGGGTTTCC 11919

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Qy 481 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGTAGCTTACA 540
Db 11980 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGTAGCTTACA 12039

Qy 541 ACTTAATCTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGGCTAGTGGCAGAGACAA 600
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Qy 601 TTCACAAACACAGCCCTTTTAAAGGGCTTAGGGATCATAAGGGGATTTTCTAGAGAGCG 660
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Qy 421 TCGGCATGACATGCTGTAAATTAATCTCCAGCATTAATCTTCTGCTTCCATTTCTTCTCTTC 480  
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Qy 481 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGACAGAACCACTGTAAGCTACA 540  
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Qy 781 TCTGAAAGTAGAAAGGTTACATTTAAGTTGCGTTGTTAGCAATTCAGTGTGTCGGA 840  
Db 12280 TCTGAAAGTAGAAAGGTTACATTTAAGTTGCGTTGTTAGCAATTCAGTGTGTCGGA 12339  
Qy 841 CCTCAGCTACAGCATCCTCGAAGCTTCCGAGGCTCCGAGACCCAGAGTTTCTCGCCCTTAGAT 900  
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Qy 901 CCAAACTTGAGCAACCCGAGTCTGGAATCTCTGGGAAGTCTCTCAGCTGTCTCGCGTTGT 960  
Db 12400 CCAAACTTGAGCAACCCGAGTCTGGAATCTCTGGGAAGTCTCTCAGCTGTCTCGCGTTGT 12459  
Qy 961 GCCGGGCCCCAGGTCTGGAGGGACCACTGCGCGTGTGGC 1001  
Db 12460 GCCGGGCCCCAGGTCTGGAGGGACCACTGCGCGTGTGGC 12500

RESULT 6

US-09-949-016-12197  
; Sequence 12197, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12197  
; LENGTH: 44952  
; TYPE: DNA

; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(44952)  
; OTHER INFORMATION: n = A, T, C or G  
US-09-949-016-12197  
  
Query Match 100.0%; Score 1001; DB 3; Length 44952;  
Best Local Similarity 100.0%; Pred. No. 3.5e-287;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGGCTGCTCGAATCTTCTGACTCTAGA 120  
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Db 131 TGATCCACCTGCTCTGCTCTCTAAAGTCTGCGGATTACAGGTGTGAGCCACCATGCGCCA 190  
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Qy 361 ATAATACCTGGGGTGTCTTCTGGGTATCAGCGATCTTCAATGAATGCCGGAGGGGTTTCC 420  
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RESULT 7  
US-09-949-016-17583  
; Sequence 17583, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CU001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17583  
; LENGTH: 44960  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(44960)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-17583  
Query Match 100.0%; Score 1001; DB 3; Length 44960;  
Best Local Similarity 100.0%; Pred. No. 3.5e-287;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCGTGGGATTACAGGCAACCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGA 60  
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Db 431 TCGCATGCATGGTGTGTTTAACTCAGCATATCTTCTGCTTCAATTTCTCTTC 490  
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Qy 721 GAGGGTGCAGGCGCTGTTCAATAGCTAGCTCCATTAATAAAGCAATTTCTCCGGCAGTT 780  
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RESULT 8  
US-09-733-294A-30  
; Sequence 30, Application US/09733294A  
; Patent No. 6492171  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: William Gaarde  
; APPLICANT: Susan M. Freier  
; APPLICANT: Edward V. Wanciewicz  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION  
; FILE REFERENCE: ISPH-0527  
; CURRENT APPLICATION NUMBER: US/09/733,294A  
; CURRENT FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: 09/572,423  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 108  
; SEQ ID NO 30  
; LENGTH: 51552  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (1)...(11492)  
; OTHER INFORMATION: exon 1  
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; OTHER INFORMATION: exon 3  
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; OTHER INFORMATION: exon 15
; LOCATION: (47174)...(47709)
; OTHER INFORMATION: intron 15
; NAME/KEY: exon
; LOCATION: (47710)...(50544)
; OTHER INFORMATION: exon 16
; US-09-733-294A-30

Query Match 97.2%; Score 972.8; DB 3; Length 51552;
Best Local Similarity 99.5%; Pred. No. 9.3e-279;
Matches 997; Conservative 0; Mismatches 2; Indels 3; Gaps 2;

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Db 9230 GGCTGGGATTACAGGCACCGCCACCATGCGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 9289

Qy 61 CGGGGGTGGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 120
Db 9290 CGGGGGT - GGGTGGGGTTTCCCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 9347

Qy 121 TGATCCACCTGCTCTGCTCTTAAAGTGTGGGATTACAGGTGTGAGGCCACCATGCCA 180
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Qy 181 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240
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Qy 241 AGTGTGTGGTGTGTTTAAAGCCAAATGATAGAAATTTTATTTGTTGTAGAAACATCTTTGA 300
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Qy 301 TGTTTACACTGTGATGACATAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
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Qy 361 ATAATACCTGGGTGCTCTTCTGGGTATCAGCGATCTTCATTAATGAAATCCGGGAGGGGTTCC 420
Db 9588 ATAATACCTGGGTGCTCTTCTGGGTATCAGCGATCTTCATTAATGAAATCCGGGAGGGGTTCC 9647

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Db 9648 TCGCCATGCACATGGTGTAAATTAATCTCCAGCATAACTCTTGCTTCCATTTCTCTCTTC 9707

Qy 481 CTTCTTTTAAATTTGTTTCTATGTTGGTTCTCTGAGAGAAACAGTGTAGCTACATA 540
Db 9708 CTTCTTTTAAATTTGTTTCTATGTTGGTTCTCTGAGAGAAACAGTGTAGCTACATA 9767

Qy 541 ACTTAACCTTTTGGGAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGACACAA 600
Db 9768 ACTTAACCTTTTGGGAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGACACAA 9827

Qy 601 TTCAAAACACACAGCCCTTTTAAAGAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCG 660
Db 9828 TTCAAAACACACAGCCCTTTTAAAGAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCG 9887

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Db 10128 TCCAACTTGAGCAACCCGAGTCTGGATTCTCGGGAAGTCCTCAGCTGCTCGGGTTG 10187  
Qy 960 TGGCGGGGCCCCAGGTCTGGAGGGGACCACTGGGCCGTGTGGC 1001  
Db 10188 TGGCGGGGCCCCAGGTCTGGAGGGGACCACTGGGCCGTGTGGC 10229

## RESULT 9

US-08-974-549A-6  
Sequence 6, Application US/08974549A  
Patent No. 6166178  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4335 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
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US-08-974-549A-6  
Query Match 93.0%; Score 930.8; DB 3; Length 4335;  
Best Local Similarity 99.1%; Pred. No. 9.7e-267; Mismatches 2; Indels 7; Gaps 6;  
Matches 999; Conservative 0;  
Qy 1 GGCTGGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTGTATTTAGTAGAGA 60  
Db 438 GGCTGGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTGTATTTAGTAGAGA 497  
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Qy 181 GCTCAGAAATTTACTCTGTTTGTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240  
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Qy 361 ATAATACTGGGGTGTCTTCTGGGTATCAGCGATCTTCAATGAATGCCGGAGGGGTTTCC 420  
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Qy 541 ACTTAACCTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTTGGCCTAGTGGCAGAGCAA 600  
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Qy 601 TTCAAAACACAGCCCTTTTAAAGGCTTAGGATGATCTAAGGGGATTTCTAGAGAGCG 660  
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US-09-721-456-6

; Sequence 6, Application US/09721456

; Patent No. 6617110

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin B.

; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/721,456

; FILING DATE: 22-No. 6617110-2000

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,549A

; FILING DATE: 19-NOV-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4335 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
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; LOCATION: 4173..4326  
; OTHER INFORMATION: /note= "intron 2"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-721-456-6

Query Match 93.0%; Score 930.8; DB 3; Length 4335;

Best Local Similarity 99.1%; Pred. No. 9.7e-267;

Matches 999; Conservative 0; Mismatches 2; Indels 7; Gaps 6;

Qy 1 GGCTGGGATTACAGGCACCGCCACCATGCCAGCAATATTTTGTATTTTAGTAGAGA 60  
Db 438 GGCTGGGATTACAGGCACCGCCACCATGCCAGCAATATTTTGTATTTTAGTAGAGA 497  
Qy 61 CGGGGGTGGGGTGGGGTTACCAATGTGGCCAGGCTGTCTCGAACTTCTGACCTCAGA 120  
Db 498 CGGGGGTGGGGTGGGGTTACCAATGTGGCCAGGCTGTCTCGAACTTCTGACCTCAGA 557  
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Db 918 CCTCTTTTAAATTTGTGTTTTCTATGTTGGCTTCTCTCAGAGAACCACTGTAGCTACA 977

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Qy 1398 CGGTTGTGCCGGGCCCCAGGCTCTGGAGGGGACACAGTGGCGCGTGTGGC 1445
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## RESULT 11

US-09-956-335-2/c

; Sequence 2, Application US/09956335

; Patent No. 6627190

; GENERAL INFORMATION:

; APPLICANT: WOLD, William

; APPLICANT: TOTH, Karoly

; APPLICANT: KUPPASWAMI, Mohan

; APPLICANT: DORONIN, Konsantini

; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE

; FILE REFERENCE: 16153-8394

; CURRENT APPLICATION NUMBER: US/09/956,335

; CURRENT FILING DATE: 2001-09-19

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 35871

; TYPE: DNA

; ORGANISM: Adenovirus

US-09-956-335-2

Query Match 67.7%; Score 677.8; DB 3; Length 35871;

Best Local Similarity 99.7%; Pred. No. 5.7e-191;

Matches 679; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 35713 AAGTAATCATCAGCTTTTCAAAGACACACTAACTGACCCCATATACTATCTGGGGTGTCTCT 35654
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Qy 35653 GGGTATCAGCGAATCTTCAATGAATGCCGGAGGCGTTTCTCGCATGCAATGGTGTTA 35594
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Qy 35593 ATTACTCCAGCATATCTTCTGCTTCCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 35534
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Qy 501 TCTATGTGGCTTCTCTGACAGAACCAAGTGTAGCTTAACTTAACTTTTGTGGAAACA 560
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Db 35533 TCTATGTGGCTTCTCTGACAGAACCAAGTGTAGCTTAACTTAACTTTTGTGGAAACA 35474
Qy 561 AATTTTCCAAACCGCCCTTTTGGCCCTAGTGGCAGAGCAATTCACAAACACAGCCCTTTTA 620
Db |||||||
Qy 35473 AATTTTCCAAACCGCCCTTTTGGCCCTAGTGGCAGAGCAATTCACAAACACAGCCCTTTTA 35414
Db |||||||
Qy 621 AAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAAGGCGACCCGTTAATCCTAAGTATTT 680
Db |||||||
Qy 35413 AAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAAGGCGACCCGTTAATCCTAAGTATTT 35354
Db |||||||
Qy 681 ACAAGACGAGGCTTAACCTCCAGCGAGCGTGACAGCCCGAGGAGGGTGCAGAGCCCTGTTC 740
Db |||||||
Qy 35353 ACAAGACGAGGCTTAACCTCCAGCGAGCGTGACAGCCCGAGGAGGGTGCAGAGCCCTGTTC 35294
Db |||||||
Qy 741 AATGCTAGCTCCATAATAAAGCAATTTCTCCGGCAGTTTCTGAAAGTAGGAAGGTTA 800
Db |||||||
Qy 35293 AATGCTAGCTCCATAATAAAGCAATTTCTCCGGCAGTTTCTGAAAGTAGGAAGGTTA 35234
Db |||||||
Qy 801 CATTTAAGGTTGCGTTTGTAGCATTTTCAAGTGTGGCGACCTCAGCTACAGCATCCCTG 860
Db |||||||
Qy 35233 CATTTAAGGTTGCGTTTGTAGCATTTTCAAGTGTGGCGACCTCAGCTACAGCATCCCTG 35174
Db |||||||
Qy 861 CAAGGCTCCGGAGACCCAGCAAGTTTCTCGCCCTTAGATCCAAACTTGAGCAACCCGGA 920
Db |||||||
Qy 35173 CAAGGCTCCGGAGACCCAGCAAGTTTCTCGCCCTTAGATCCAAACTTGAGCAACCCGGA 35114
Db |||||||
Qy 921 GTCTGATTCCTGGGAAGTCTCAGCTGTCTCGGGTGTGCGGGGCCCCAGGTCGTGGA 980
Db |||||||
Qy 35113 GTCTGATTCCTGGGAAGTCTCAGCTGTCTCGGGTGTGCGGGGCCCCAGGTCGTGGA 35054
Db |||||||
Qy 981 GGGGACCAAGTGGCGGTGTGGC 1001
Db |||||||
Qy 35053 GGGGACCAAGTGGCGGTGTGGC 35033
Db |||||||
```

## RESULT 12

US-09-956-335-1/c

; Sequence 1, Application US/09956335

; Patent No. 6627190

; GENERAL INFORMATION:

; APPLICANT: WOLD, William

; APPLICANT: TOTH, Karoly

; APPLICANT: KUPPASWAMI, Mohan

; APPLICANT: DORONIN, Konsantini

; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE

; FILE REFERENCE: 16153-8394

; CURRENT APPLICATION NUMBER: US/09/956,335

; CURRENT FILING DATE: 2001-09-19

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 35978

; TYPE: DNA

; ORGANISM: Adenovirus

US-09-956-335-1

Query Match 67.7%; Score 677.8; DB 3; Length 35978;

Best Local Similarity 99.7%; Pred. No. 5.7e-191;

Matches 679; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 321 AAGCATCATCAGCTTTTCAAAGACACACTAACTGACCCCATATACTATCTGGGGTGTCTCT 380
Db |||||||
Qy 35820 AAGTAATCATCAGCTTTTCAAAGACACACTAACTGACCCCATATACTATCTGGGGTGTCTCT 35761
Db |||||||
Qy 381 GGGTATCAGCGAATCTTCAATGAATGCCGGAGGCGTTTCTCGCATGCAATGGTGTTA 440
Db |||||||
Qy 35760 GGGTATCAGCGAATCTTCAATGAATGCCGGAGGCGTTTCTCGCATGCAATGGTGTTA 35701
Db |||||||
Qy 441 ATTACTCCAGCATATCTTCTGCTTCCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 500
Db |||||||
Qy 35700 ATTACTCCAGCATATCTTCTGCTTCCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 35641
Db |||||||
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Qy 501 TCTATGTTGGCTTCTCTGAGAGAACAGTGTAAAGTACAACTTAACTTTTGTGGACA 560  
Db |||||  
35640 TCTATGTTGGCTTCTCTGAGAGAACAGTGTAAAGTACAACTTAACTTTTGTGGACA 35581  
Qy 561 AATTTTCAAACCGCCCTTTGCGCTAGTGGAGAGACAATTCACAAACACAGCCCTTTA 620  
Db |||||  
35580 AATTTTCAAACCGCCCTTTGCGCTAGTGGAGAGACAATTCACAAACACAGCCCTTTA 35521  
Qy 621 AAAAGGCTTAGGGATCCTAAGAGGATTTCTAGAGAGCGACCCGTAACTCCTAAGTATTT 680  
Db |||||  
35520 AAAAGGCTTAGGGATCCTAAGAGGATTTCTAGAGAGCGACCCGTAACTCCTAAGTATTT 35461  
Qy 681 ACAAGAGAGGCTTAACCTCCAGCGAGCTGACAGCCCAAGGAGGGTGGAGGCTTTTCA 740  
Db |||||  
35460 ACAAGAGAGGCTTAACCTCCAGCGAGCTGACAGCCCAAGGAGGGTGGAGGCTTTTCA 35401  
Qy 741 AATGCTAGCTCATATAATAAGCAATTTCTCCGCGAGTTCCTGAAAGTAAAGGTTA 800  
Db |||||  
35400 AATGCTAGCTCATATAATAAGCAATTTCTCCGCGAGTTCCTGAAAGTAAAGGTTA 35341  
Qy 801 CAATTAAGGTTGCGTTTGTAGCAATTTCCAGTGTGTTGCGGAGCTCAGCTACAGCATCCCTG 860  
Db |||||  
35340 CAATTAAGGTTGCGTTTGTAGCAATTTCCAGTGTGTTGCGGAGCTCAGCTACAGCATCCCTG 35281  
Qy 861 CAAGGCTCGGGAGACCCAGAAATTTCTCGGCCCTTAGATCCAACTTGAGCAACCCGGA 920  
Db |||||  
35280 CAAGGCTCGGGAGACCCAGAAATTTCTCGGCCCTTAGATCCAACTTGAGCAACCCGGA 35221  
Qy 921 GTCTGGATCTCGGAAGTCTCAGCTGTCTGCGGTTGTCGCGGGCCCGAGGTCTGGA 980  
Db |||||  
35220 GTCTGGATCTCGGAAGTCTCAGCTGTCTGCGGTTGTCGCGGGCCCGAGGTCTGGA 35161  
Qy 981 GGGGACCAAGTGGCGTGTGGC 1001  
Db |||||  
35160 GGGGACCAAGTGGCGTGTGGC 35140

## RESULT 13

US-09-956-335-3/c  
; Sequence 3, Application US/09956335  
; Patent No. 6627190  
; GENERAL INFORMATION:  
; APPLICANT: WOLD, William  
; APPLICANT: TOTH, Karoly  
; APPLICANT: KUPPASHWAMI, Mohan  
; APPLICANT: DORONIN, Konstantin  
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE  
; FILE REFERENCE: 16153-8394  
; CURRENT APPLICATION NUMBER: US/09/956,335  
; CURRENT FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 3  
; TYPE: DNA  
; ORGANISM: Adenovirus  
US-09-956-335-3

Query Match 67.5%; Score 676; DB 3; Length 1677;  
Best Local Similarity 100.0%; Pred. No. 4.8e-191;  
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 326 ATCATCAGCTTTTCAAAGACACACTAACTGACCCCAATAATACTGGGGTGTCTCTGGGTA 385  
Db 1676 ATCATCAGCTTTTCAAAGACACACTAACTGACCCCAATAATACTGGGGTGTCTCTGGGTA 1617  
Qy 386 TCAGGATCTTCATTAAGTGGGAGGGGTTCTCGCCATGACATGGTGTAAATTAC 445  
Db 1616 TCAGGATCTTCATTAAGTGGGAGGGGTTCTCGCCATGACATGGTGTAAATTAC 1557  
Qy 446 TCCAGCAATCTCTGCTTCATTTCTCTCTCCCTCTTTTAAATTTGTTTCTAT 505

Db 1556 TCCAGCAATCTCTGCTTCCATTTCTCTCTCCCTCTTTTAAATTTGTTTCTAT 1497  
Qy 506 GTTGGCTTCTCTGAGAGAACAGTGTAAAGTACAACTTAACTTTTGTGGACAATAATTT 565  
Db 1496 GTTGGCTTCTCTGAGAGAACAGTGTAAAGTACAACTTAACTTTTGTGGACAATAATTT 1437  
Qy 566 TCCAAAACCGCCCTTTTGGCTAGTGGAGAGACAATTCACAAACACAGCCCTTTTAAAAAG 625  
Db 1436 TCCAAAACCGCCCTTTTGGCTAGTGGAGAGACAATTCACAAACACAGCCCTTTTAAAAAG 1377  
Qy 626 GCTTAGGATCACAATAAGGGATTTCTAGAGAGCGACCCGTAACTCCTAAGTATTTACAAG 685  
Db 1376 GCTTAGGATCACAATAAGGGATTTCTAGAGAGCGACCCGTAACTCCTAAGTATTTACAAG 1317  
Qy 686 ACAGAGGCTTAACCTCCAGCGAGCTGACAGCCCAAGGAGGGTGGAGGCTTTTCAAAATGC 745  
Db 1316 ACAGAGGCTTAACCTCCAGCGAGCTGACAGCCCAAGGAGGGTGGAGGCTTTTCAAAATGC 1257  
Qy 746 TAGCTCCATAATAATAAGCAATTTCTCCGCGAGTTCCTGAAAGTAGGAAAGGTTACATTT 805  
Db 1256 TAGCTCCATAATAATAAGCAATTTCTCCGCGAGTTCCTGAAAGTAGGAAAGGTTACATTT 1197  
Qy 806 AAGTGGCTTGTAGCAATTTCTAGTGTTCGCGACCTCAGCTACAGCATCCCTGCAAGG 865  
Db 1196 AAGTGGCTTGTAGCAATTTCTAGTGTTCGCGACCTCAGCTACAGCATCCCTGCAAGG 1137  
Qy 866 CCTCGGAGACCCAGAAATTTCTCGGCCCTTAGATCCAACTTGAGCAACCCGAGTCTG 925  
Db 1136 CCTCGGAGACCCAGAAATTTCTCGGCCCTTAGATCCAACTTGAGCAACCCGAGTCTG 1077  
Qy 926 GATTCTCTGGGAAGTCTCAGCTGTCTGCGGTTGTCGCGGGCCCGAGGTCTGGAGGGGA 985  
Db 1076 GATTCTCTGGGAAGTCTCAGCTGTCTGCGGTTGTCGCGGGCCCGAGGTCTGGAGGGGA 1017  
Qy 986 CCAGTGGCGGTGTGGC 1001  
Db 1016 CCAGTGGCGGTGTGGC 1001

## RESULT 14

US-09-244-438-22  
; Sequence 22, Application US/09244438  
; Patent No. 6777203  
; GENERAL INFORMATION:  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Lichtsteiner, Serge  
; APPLICANT: Vasserot, Alain  
; APPLICANT: Adams, Robert R.  
; APPLICANT: Geron Corporation  
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional  
; FILE REFERENCE: 019/246P  
; CURRENT APPLICATION NUMBER: US/09/244,438  
; CURRENT FILING DATE: 1999-02-04  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 497  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human TERT promoter  
US-09-244-438-22

Query Match 49.7%; Score 497; DB 3; Length 497;  
Best Local Similarity 100.0%; Pred. No. 5.6e-138;  
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 444 ACTCAGCATTAATCTCTGCTTCCATTTCTCTCTCCCTCTTTTAAATTTGTGTTTCT 503  
Db 1 ACTCAGCATTAATCTCTGCTTCCATTTCTCTCTCTCCCTCTTTTAAATTTGTGTTTCT 60  
Qy 504 ATGTTGGCTTCTCTGAGAGAACAGTGTAAAGTACAACTTAACTTTTGTGGACAAT 563

[illegible]

## RESULT 15

```

RES001 13
US-08-912-951-6
; Sequence 6, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
;

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[illegible]

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Qy 659 CGACCCGTAATCCTAAGTATTACAGACGAGGCTAACCTCAGCGAGCGTGACAGCCA 718
Db 1132 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Qy 719 GGGAGGGTGCAGGCGCTGTTCAAAATGTAGTCTCATAAATAAGCAAATTTCTCCGGCAG 778
Db 1192 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Qy 779 TTTCTGAAAGTAGGAAAGGTTACATTAAAGGTTGGGTTGTAGCATTTTCAGTGTGGCC 838
Db 1252 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Qy 839 GACCTCAGCTACAGCATCCCTGCAAGGCTCGGAGAGCCAGAAAGTTTCTCGCCCTTAG 898
Db 1312 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Qy 899 ATCCAAACTTGAGCAACCCGAGTCTGGATTCTGGGGAAGTCTCAGCTGTCTGCGGTT 958
Db 1372 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Qy 959 GTGCGGGGGCCCGAGTCTGGAG 981
Db 1432 GNNRGAGGGGCCANGRAGGGGG 1454
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Job time : 208 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 05:46:59 ; Search time 690.667 Seconds  
(without alignments)  
9659.301 Million cell updates/sec

Title: US-09-615-039-1\_COPY\_11500\_12500

Perfect score: 1001

Sequence: 1 ggctggattacagcacc.....gggaccagtggcgtgtggc 1001

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq\_21.\*

- 1: geneseqn1980s.\*
- 2: geneseqn1990s.\*
- 3: geneseqn2000s.\*
- 4: geneseqn2001as.\*
- 5: geneseqn2001bs.\*
- 6: geneseqn2002as.\*
- 7: geneseqn2002bs.\*
- 8: geneseqn2003as.\*
- 9: geneseqn2003bs.\*
- 10: geneseqn2003cs.\*
- 11: geneseqn2003ds.\*
- 12: geneseqn2004as.\*
- 13: geneseqn2004bs.\*
- 14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1001	100.0	15418	3	AA63785 Nucleotide
2	1001	100.0	15418	6	Aa138601 Human TER
3	1001	100.0	15418	6	AB54997 Lambda cl
4	1001	100.0	15418	6	Aa138595 DNA of pl
5	1001	100.0	15418	10	Adc21253 Lambda cl
6	989	98.8	3962	4	Aa41091 Telomeras
7	989	98.8	4356	13	Adu82633 Human hTE
8	988.6	98.8	4293	14	Adv23865 Human hTE
9	972.8	97.2	5491	13	Adu82631 Human hTE
10	972.8	97.2	51552	6	Aa96607 DNA encod
11	971.8	97.1	5126	2	Aax88272 Human cat
12	956	95.5	2501	14	Adv97952 Human tum
13	954.4	95.3	7928	14	Aa18025 Human gyn
14	930.8	93.0	4335	2	Aa16979 Human tel
15	677.8	67.7	35871	6	Aad27972 Recombina
16	677.8	67.7	35978	6	Aad27971 Recombina
17	676	67.5	1677	6	Aad27973 Human tel
18	676	67.5	2043	14	Adv23882 Human hTE
19	643.2	64.3	4356	6	Ab192335 Chemical

20	636	63.5	4356	6	ABL92334	Ab192334 Chemical
21	623.8	62.3	2501	14	ADV98043	Adv98043 Bisulfite
22	623.4	62.3	2501	14	ADV98042	Adv98042 Bisulfite
23	622.2	62.2	7928	14	AEA18047	Aea18047 Converted
24	620.2	62.0	7928	14	AEA18046	Aea18046 Converted
25	588.6	58.8	2501	14	ADV98137	Adv98137 Bisulfite
26	588.6	58.8	7928	14	AEA18067	Aea18067 Converted
27	588.2	58.8	2501	14	ADV98136	Adv98136 Bisulfite
28	586.6	58.6	7928	14	AEA18066	Aea18066 Converted
29	285.6	20.5	1404	6	AD22343	Ad22343 Chemical
30	195.6	19.5	1404	6	AD22344	Ad22344 Chemical
31	136.4	13.6	158980	13	ADZ44537	Adz44537 Human bre
32	134.2	13.4	7268	4	AAK85177	Aak85177 Human imm
33	134.2	13.4	18596	4	AAF31109	Aaf31109 Thymidyla
34	134.2	13.4	18596	5	AAC91215	Aac91215 Human thy
35	134.2	13.4	18596	6	ABL67927	Ab167927 Ovary can
36	134.2	13.4	18596	6	ABL62854	Ab162854 Breast ca
37	134.2	13.4	18596	6	ABL63078	Ab163078 Breast ca
38	134.2	13.4	18596	6	ABK43334	Abk43334 Human Thy
39	134.2	13.4	18596	6	ABN95092	Abn95092 Gene #159
40	134.2	13.4	18596	14	AEA63667	Aea63667 Thymidyla
41	134.2	13.4	45716	6	ABA93401	Aba93401 Human rTS
42	134.2	13.4	45989	6	ABA93402	Aba93402 Human rTS
43	132.8	13.3	196686	11	ACN44170	Acn44170 Human gen
44	132.2	13.2	24295	12	ADP31706	Adp31706 Human oes
45	131.4	13.1	69648	12	ADQ97934	Adq97934 Human can

## ALIGNMENTS

### RESULT 1

AAA63785

ID AAA63785 standard; DNA; 15418 BP.

XX AAA63785;

DT 04-DEC-2000 (first entry)

DE Nucleotide sequence of the human TERT promoter and gene from pGRN142.

XX Telomerase reverse transcriptase; TERT; promoter; telomerase complex;

XX telomere length; hyperplastic disease; cancer; oncolytic virus;

XX cis-acting transcriptional control sequence; viral replication;

XX cell proliferation; aging; immunological disorder; infertility; ss.

XX Homo sapiens.

XX WO200046355-A2.

XX 10-AUG-2000.

XX 04-FEB-2000; 2000WO-US003104.

XX 04-FEB-1999; 99US-00244438.

XX (GERO-) GERON CORP.

XX Morin GB, Lichtsteiner S, Vasserot A, Adams R, Cardozo LM;

XX Lebkowski JS;

XX WPI; 2000-532898/48.

XX New polynucleotides comprising cis-acting transcriptional control

XX sequences, e.g. promoter sequence, of telomerase reverse transcriptase

XX genes, useful in the treatment of cancer.

XX Claim 9; Page 58-61; 63pp; English.

XX The present sequence represents the human telomerase reverse

XX transcriptase (TERT) promoter and gene. TERT is part of the telomerase

XX complex responsible for maintaining telomere length and increasing

XX replicative capacity of progenitor cells. Telomerase activity is turned

off in mature differentiated cells, but is turned back on again in hyperplastic diseases, including many cancers. The polynucleotide comprises cis-acting, transcriptional control sequences, e.g. promoter sequences. These promoter sequences are used to produce oncolytic viruses, in which a toxin or genetic element essential for viral replication is placed under the control of a TERT promoter. As a result, the virus replicates preferentially in cells expressing TERT, and selectively lyses cancer cells. The oncolytic viruses are useful for treating cancer in humans or animals. The TERT promoter sequences are useful in the treatment of cancer and other diseases of cell proliferation such as degenerative and aging processes and diseases of aging, immunological disorders, or infertility

Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 1001; DB 3; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 6.4e-291;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTGGGATTACAGGACCCGCCACCATGCGCCAGCTAAATTTTGTATTTTAGTAGAGA 60  
DB 11500 GGCTGGGATTACAGGACCCGCCACCATGCGCCAGCTAAATTTTGTATTTTAGTAGAGA 11559

QY 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAATCTCTGACCTCAGA 120  
DB 11560 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAATCTCTGACCTCAGA 11619

QY 121 TGATCCACCTGCTCTGCCCTCCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 180  
DB 11620 TGATCCACCTGCTCTGCCCTCCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 11679

QY 181 GCTCAGAAATTACTCTGTTTAAAGCAATCTGGGTCTGAGTAGGAAGCTCACCCACTCA 240  
DB 11680 GCTCAGAAATTACTCTGTTTAAAGCAATCTGGGTCTGAGTAGGAAGCTCACCCACTCA 11739

QY 241 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTGTTTGTAGAACACTCTTGA 300  
DB 11740 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTGTTTGTAGAACACTCTTGA 11799

QY 301 TGTTTTACATGTGATGACATAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360  
DB 11800 TGTTTTACATGTGATGACATAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 11859

QY 361 ATAATACATGGGGTCTCTTGGGTATCAGCATCTTCATTTGAATCCGGGAGGGTTTCC 420  
DB 11860 ATAATACATGGGGTCTCTTGGGTATCAGCATCTTCATTTGAATCCGGGAGGGTTTCC 11919

QY 421 TCGCATGCATGGTGTAAATTAATCTCAGCATATCTTCTGCTTCCATTTCTTCTCTTC 480  
DB 11920 TCGCATGCATGGTGTAAATTAATCTCAGCATATCTTCTGCTTCCATTTCTTCTCTTC 11979

QY 481 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTTCGAGAGAACAGTGTAGTACATA 540  
DB 11980 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTTCGAGAGAACAGTGTAGTACATA 12039

QY 541 ACTTAATCTTTTGGGAACAAATTTTCAAACCCCTTGGCTTGGCTAGTGGCAGACAA 600  
DB 12040 ACTTAATCTTTTGGGAACAAATTTTCAAACCCCTTGGCTTGGCTAGTGGCAGACAA 12099

QY 601 TTCAAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAAGAGCG 660  
DB 12100 TTCAAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAAGAGCG 12159

QY 661 ACCCGTAATCTTAAGTATTTTAAAGACGAGCTTAACCTCCAGCGAGCGTGACAGCCGAGG 720  
DB 12160 ACCCGTAATCTTAAGTATTTTAAAGACGAGCTTAACCTCCAGCGAGCGTGACAGCCGAGG 12219

QY 721 GAGGGTCGAGGCTGTTTCAATCTAGTCCATAAATAAGCAATTTTCTCCGGCAGTT 780  
DB 12220 GAGGGTCGAGGCTGTTTCAATCTAGTCCATAAATAAGCAATTTTCTCCGGCAGTT 12279

QY 781 TCTCAAAAGTAGGAAGGTTTCAATTTAAGGTTGCGTTTGTAGCATTTTCAGTGTGTCGGA 840

DB 12280 TCTGAAAGTAGGAAGGTTTACATTTAAAGTGTGCGTTTGTAGCATTTTCAGTGTGTCGGA 12339

QY 841 CCTCAGCTACAGCATCCCTGCAAGGCTCTGGGAGACCCAGAAAGTTTCTGCCCCCTTAGAT 900

DB 12340 CCTCAGCTACAGCATCCCTGCAAGGCTCTGGGAGACCCAGAAAGTTTCTGCCCCCTTAGAT 12399

QY 901 CCAAACTTTCAGCAACCCCGAGTCTGATTTCTTGGGAAGTCTCAGCTGTCTCGGGTTGT 960

DB 12400 CCAAACTTTCAGCAACCCCGAGTCTGATTTCTTGGGAAGTCTCAGCTGTCTCGGGTTGT 12459

QY 961 GCCGGGGCCCCAGTCTGAGGGGACCAGTGGCGCGTGTG3C 1001

DB 12460 GCCGGGGCCCCAGTCTGAGGGGACCAGTGGCGCGTGTG3C 12500

RESULT 2  
AAL38601  
ID AAL38601 standard; DNA; 15418 BP.  
XX  
AC AAL38601;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
Human TERT promoter and upstream sequence.  
XX  
Cytostatic; glycosyltransferase; tumour; cell-surface carbohydrate;  
KW tissue specific; transcriptional control element; cancer cell;  
KW gene therapy; human TERT; telomerase reverse transcriptase; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200242468-A2.  
XX  
PD 30-MAY-2002.  
XX  
PF 26-NOV-2001; 2001WO-US044306.  
XX  
PR 27-NOV-2000; 2000US-0253395P.  
XX  
(GERO-) GERON CORP.  
XX  
Schiiff MJ;  
XX  
WPI; 2002-479954/51.  
XX  
New polynucleotide encoding glycosyltransferase enzymes including histo  
PT blood group transferase useful for treating conditions associated with  
PT hyperproliferation, such as cancers and other neoplasias.  
XX  
Claim 9; Page 17-20; 49pp; English.

The invention relates to a polynucleotide comprising an encoding sequence for a glycosyltransferase, under control of a heterologous tumour specific or tissue specific transcriptional control element, where expression of the polynucleotide in a human cell causes the cell to express a cell-surface carbohydrate determinant to which some or all humans have a naturally occurring antibody. The polynucleotide of the invention is useful for killing cancer cells and for preparing a medicament for the treatment of cancer. The polynucleotide sequence of the invention can be used to treat disorders by gene therapy. This polynucleotide sequence represents the human TERT (telomerase reverse transcriptase) promoter and upstream sequence related to the invention

Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 1001; DB 6; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 6.4e-291;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTGGGATTACAGGACCCGCCACCATGCGCCAGCTAAATTTTGTATTTTAGTAGAGA 60  
DB 11500 GGCTGGGATTACAGGACCCGCCACCATGCGCCAGCTAAATTTTGTATTTTAGTAGAGA 11559





Db 11500 GGCCTGGATTACAGGACCCGCCACCATGCCACGCTAATTTTTTGATTTTTTAGTAGAGA 11559  
Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTGGCCAGCTGGTTCGAACTTCTGACCTCAGA 120  
Db 11560 CGGGGGTGGGGTGGGGTTCACCATGTGGCCAGCTGGTTCGAACTTCTGACCTCAGA 11619  
Qy 121 TGATCCACCTGCTCTGCTCCCTTAAGTCTGGGATTTACAGGTGTGAGCCACCATGCCCA 180  
Db 11620 TGATCCACCTGCTCTGCTCCCTTAAGTCTGGGATTTACAGGTGTGAGCCACCATGCCCA 11679  
Qy 181 GCTCAGAAATTACCTCTGTTTGTAGAAACATCTGGGCTCAGGTTGAGGAAGCTCACCCCACTCA 240  
Db 11680 GCTCAGAAATTACCTCTGTTTGTAGAAACATCTGGGCTCAGGTTGAGGAAGCTCACCCCACTCA 11739  
Qy 241 AGTGTGTGGTGTGTTTTAAGCAATGATAGAAATTTTTTTTATTTGTTTGTAGAACACTCTTGA 300  
Db 11740 AGTGTGTGGTGTGTTTTAAGCAATGATAGAAATTTTTTTTATTTGTTTGTAGAACACTCTTGA 11799  
Qy 301 TGTTTTACATGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360  
Db 11800 TGTTTTACATGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 11859  
Qy 361 ATAATACCTGGGGTCTCTTCTGGGTATCAGCATCTTCATTGAATGCCGGAGGGGTTTCC 420  
Db 11860 ATAATACCTGGGGTCTCTTCTGGGTATCAGCATCTTCATTGAATGCCGGAGGGGTTTCC 11919  
Qy 421 TCGCATGCAATGGTGTAAATTAATCTCCAGCATAACTTCTGCTTCCATTTCTTCTCTTC 480  
Db 11920 TCGCATGCAATGGTGTAAATTAATCTCCAGCATAACTTCTGCTTCCATTTCTTCTCTTC 11979  
Qy 481 CCTCTTTTAAATTTGTTTCTATGTTGGTCTTCTGCGAGAACACAGTGTAGCTACA 540  
Db 11980 CCTCTTTTAAATTTGTTTCTATGTTGGTCTTCTGCGAGAACACAGTGTAGCTACA 12039  
Qy 541 ACTTAACCTTTGTTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGCAGAGACAA 600  
Db 12040 ACTTAACCTTTGTTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGCAGAGACAA 12099  
Qy 601 TTCAAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAAGCG 660  
Db 12100 TTCAAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAAGCG 12159  
Qy 661 ACCGTAATCTTAAGTATTTACAAGACGAGCTTAACCTCCAGCGAGGTGACAGCCGAG 720  
Db 12160 ACCGTAATCTTAAGTATTTACAAGACGAGCTTAACCTCCAGCGAGGTGACAGCCGAG 12219  
Qy 721 GAGGGTCCGAGGCTGTTCAAATGCTAGCTCCATAAATAAGCAATTTCTCCGGCAGTT 780  
Db 12220 GAGGGTCCGAGGCTGTTCAAATGCTAGCTCCATAAATAAGCAATTTCTCCGGCAGTT 12279  
Qy 781 TCTGAAAGTAGGAAGGTACATTTAAGGTTGCGTTTGTGTAGCAATTTCAAGTTTTCGCGA 840  
Db 12280 TCTGAAAGTAGGAAGGTACATTTAAGGTTGCGTTTGTGTAGCAATTTCAAGTTTTCGCGA 12339  
Qy 841 CCTCAGCTACAGCATCTCTGCAAGGCTTCGGAGACCCAGAGTTTCTCGCCCTTAGAT 900  
Db 12340 CCTCAGCTACAGCATCTCTGCAAGGCTTCGGAGACCCAGAGTTTCTCGCCCTTAGAT 12399  
Qy 901 CCAACTTGTAGCAACCCGAGTCTGGATTTCTGGAAGTCTCTCAGCTGTCTCGGGTTGT 960  
Db 12400 CCAACTTGTAGCAACCCGAGTCTGGATTTCTGGAAGTCTCTCAGCTGTCTCGGGTTGT 12459  
Qy 961 GCCGGGGCCCCAGGTCTGGAGGGGACCAAGTGGCGTGTGGC 1001  
Db 12460 GCCGGGGCCCCAGGTCTGGAGGGGACCAAGTGGCGTGTGGC 12500

RESULT 4  
AAL38595  
ID AAL38595 standard; DNA; 15418 BP.  
XX  
AC AAL38595;

XX  
DT 16-AUG-2002 (first entry)  
XX  
DE DNA of plasmid pGRN144 containing human hTERT gene.  
XX  
KW Anticonvulsant; cerebroprotective; vasotropic; nootropic; stem cell;  
KW neuroprotective; antiparkinsonian; antiinflammatory; undifferentiated;  
KW cardant; transcriptional control element; human embryonic; tissue graft;  
KW regenerative medicine; tissue reconstruction; neural progenitor cell;  
KW nerve system; epilepsy; stroke; ischaemia; Huntington's disease;  
KW Parkinson's disease; multiple sclerosis; leukodystrophy; neuritis;  
KW hepatocyte; liver damage; cardiomyocyte; cryoinjury; cardiac muscle;  
KW pGRN144; human hTERT gene; chimeric; ds.  
XX  
OS Homo sapiens.  
OS Unidentified.  
OS Chimeric.  
XX  
XX WO200242445-A2.  
XX  
XX 30-MAY-2002.  
XX  
XX 26-NOV-2001; 2001WO-US044309.  
XX  
XX 27-NOV-2000; 2000US-0253357P.  
XX 27-NOV-2000; 2000US-0253443P.  
XX 13-FEB-2001; 2001US-00783203.  
XX  
XX (GERO-) GERON CORP.  
XX  
XX Gold JD, Lebrowski JS;  
XX WPI; 2002-479952/51.  
XX  
XX Depleting a cell e.g., human embryonic stem cell population of  
XX undifferentiated stem cells (UC) for use in regenerative medicine  
XX comprises genetically altering UC in a population to express nucleic acid  
XX encoding a lethal product.  
XX  
XX Example 9; Page 62-66; 67pp; English.  
XX  
XX The invention relates to a system for depleting a cell population of  
XX undifferentiated stem cells, by introducing nucleic acids of structure P-  
XX X, where X is a nucleic acid encoding product that is lethal to a cell in  
XX which it is expressed; or renders a cell in which it is expressed  
XX susceptible to the lethal effect of an external agent, and P is a  
XX transcriptional control element causing X to be preferentially expressed  
XX in the undifferentiated stem cells. The system is used for depleting a  
XX cell population (preferably, human embryonic stem cells) of  
XX undifferentiated stem cells. A population of differentiated cells is  
XX useful in regenerative medicine, and for preparing antibodies and cDNA  
XX libraries that are specific for a differentiated phenotype. The cell  
XX populations are also useful for drug screening and therapeutic  
XX applications. The differentiated cells are useful for tissue  
XX reconstitution or regeneration in a human patient in need of treatment.  
XX The cells are administered in a manner that permits to graft to the  
XX intended tissue side and reconstitute or regenerate the functionally  
XX deficient area. The neural progenitor cells are useful for treating acute  
XX or chronic damage to the nerve system e.g. epilepsy, stroke, ischaemia,  
XX Huntington's disease, Parkinson's disease, multiple sclerosis,  
XX leukodystrophies, neuritis, etc. The hepatocytes and hepatocyte  
XX precursors are useful for assessing animal models for ability to repair  
XX liver damage. The cardiomyocyte population is useful for assessing animal  
XX models for cryoinjury, regenerating cardiac muscle and to treat  
XX insufficient cardiac function. This polynucleotide sequence represents  
XX the DNA of plasmid pGRN144 containing the human hTERT gene relating to  
XX the invention  
XX  
XX Sequence 15418 BP; 4519 A; 3797 C; 3764 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 1001; DB 6; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 6.4e-291;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GGCTGGGATTTACAGGCACCCGCCACATGCCCCAGCTAAATTTTGTATTTTGTATTTTGTAGTAGAGA	60
Db	11500	GGCTGGGATTTACAGGCACCCGCCACATGCCCCAGCTAAATTTTGTATTTTGTATTTTGTAGTAGAGA	11559
Qy	61	CGGGGGTGGGGGTGGGGTTTCCATGTTTGGCCAGAGCTGCTTCGAACTTCTCGACTCTCAGA	120
Db	11560	CGGGGGTGGGGGTGGGGTTTCCATGTTTGGCCAGAGCTGCTTCGAACTTCTCGACTCTCAGA	11619
Qy	121	TGATCCACTGCTGCTTCGCTCTCTTAAGTGTCTGGGATTACAGGTGTGAGCCACCAATGCCCCA	180
Db	11620	TGATCCACTGCTGCTTCGCTCTCTTAAGTGTCTGGGATTACAGGTGTGAGCCACCAATGCCCCA	11679
Qy	181	GCTTCAGAAATTACTCTGTGTTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA	240
Db	11680	GCTTCAGAAATTACTCTGTGTTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA	11739
Qy	241	AGTGTGTGGTGTGTTTTAAGCCCAATGATAGAAATTTTTTATTGTTGTTAGAACTCTTTGA	300
Db	11740	AGTGTGTGGTGTGTTTTAAGCCCAATGATAGAAATTTTTTATTGTTGTTAGAACTCTTTGA	11799
Qy	301	TGTTTTACACTGTGATGATCAATGACATCATCAGCTTTTCAAGACACACTAATGTCACCC	360
Db	11800	TGTTTTACACTGTGATGATCAATGACATCATCAGCTTTTCAAGACACACTAATGTCACCC	11859
Qy	361	ATAATACTCGGGGTGCTTCTCTGGGTATCAGCGATCTTCAATTGAATGCCGGGAGGGGTTTTCC	420
Db	11860	ATAATACTCGGGGTGCTTCTCTGGGTATCAGCGATCTTCAATTGAATGCCGGGAGGGGTTTTCC	11919
Qy	421	TGCGCATGACATGTGTGTTAAATTACTCCAGATATAATCTTCTGCTTCCATTTTCTCTCTTC	480
Db	11920	TGCGCATGACATGTGTGTTAAATTACTCCAGATATAATCTTCTGCTTCCATTTTCTCTCTTC	11979
Qy	481	CTCTCTTTTAAATATGTGTGTTTTCTATGTTGGCTTCTCTGCAGAGAACCAGTGTAACTACA	540
Db	11980	CTCTCTTTTAAATATGTGTGTTTTCTATGTTGGCTTCTCTGCAGAGAACCAGTGTAACTACA	12039
Qy	541	ACTTAATCTTTGTGTGAAACAAATTTTCCAAAACGGCCCCCTTGGCTTAGTGGCAGAGACAA	600
Db	12040	ACTTAATCTTTGTGTGAAACAAATTTTCCAAAACGGCCCCCTTGGCTTAGTGGCAGAGACAA	12099
Qy	601	TTCACAAAACACAGCCCTTTAAAGAGCTTAGGGATACACTAAGGGGATTTCTAGAGAGCG	660
Db	12100	TTCACAAAACACAGCCCTTTAAAGAGCTTAGGGATACACTAAGGGGATTTCTAGAGAGCG	12159
Qy	661	ACCCGTAATCTTAAGTAATTTACAAGACGAGGCTTAACCTCCACGCGAGCGTGAAGCCCAAG	720
Db	12160	ACCCGTAATCTTAAGTAATTTACAAGACGAGGCTTAACCTCCACGCGAGCGTGAAGCCCAAG	12219
Qy	721	GAGGGTCGAGGCCCTGTTCAATGCTAGCTCCATATAATAAGCAATTTTCTCCGCGAGTT	780
Db	12220	GAGGGTCGAGGCCCTGTTCAATGCTAGCTCCATATAATAAGCAATTTTCTCCGCGAGTT	12279
Qy	781	TCTCAAAAGTAGGAAAGGTTTACATTTAAGGTGCGTTTTGTTAGCATTTTCAAGTGTGTCGGA	840
Db	12280	TCTCAAAAGTAGGAAAGGTTTACATTTAAGGTGCGTTTTGTTAGCATTTTCAAGTGTGTCGGA	12339
Qy	841	CCTCAGCTACAGCATCCCTGCAAGGCCTCGGAGACCCGAGAAGTTTCTCGCCCCCTTAGAT	900
Db	12340	CCTCAGCTACAGCATCCCTGCAAGGCCTCGGAGACCCGAGAAGTTTCTCGCCCCCTTAGAT	12399
Qy	901	CCAAACTTGAGCAACCCGAGTCTGATATTCCTGGGAAGTCCCTCAGCTGTCTGCGGTTGT	960
Db	12400	CCAAACTTGAGCAACCCGAGTCTGATATTCCTGGGAAGTCCCTCAGCTGTCTGCGGTTGT	12459
Qy	961	GCCGGGGCCCCAGGCTGTGAGGGGGAACAGTGGCCGTGTGGC	1001
Db	12460	GCCGGGGCCCCAGGCTGTGAGGGGGAACAGTGGCCGTGTGGC	12500

RESULT 5  
ADC21253  
ID ADC:

XX ADC21253;  
XX AC  
XX DT 18-DEC-2003 (first entry)  
XX DE  
XX DE Lambda clone (lambdaGphi5) containing human TERT DNA.  
XX KW  
XX KW Viral vector; heterologous control element; gene expression;  
XX KW human telomerase reverse transcriptase; hTERT; tumour specific gene;  
XX KW cell death; transcriptional control element;  
XX KW human telomerase RNA component; hTR; cancer cell; liver cancer;  
XX KW prostate cancer; muscle cancer; neural cell cancer; lung cancer;  
XX KW pancreatic cancer; medulloblastoma; cervical carcinoma; fibrosarcoma;  
XX KW osteosarcoma; lambda clone; lambdaGphi5; human; ds.  
XX XX  
XX Synthetic.  
XX OS Homo sapiens.  
XX OS Bacteriophage lambda.  
XX OS  
XX PN US2003099616-A1.  
XX XX  
XX PD 29-MAY-2003.  
XX XX  
XX XX 25-JUL-2002; 2002US-00206447.  
XX XX  
XX XX 25-JUL-2001; 2001US-0308029P.  
XX XX  
XX XX (IRV1/) IRVING J M.  
XX PA (KARP/) KARPFF D B.  
XX PA (SCH1/) SCHIFF J M.  
XX XX  
XX PI Irving JM, Karpf DB, Schiff JM;  
XX DR WFI; 2003-730140/69.  
XX XX  
XX PT New dual specificity vectors driven by the telomerase promoter, useful  
XX PT for killing or slowing the growth of tumor cells, or for treating cancer,  
XX PT e.g. liver cancer, prostate cancer, lung cancer, or pancreatic cancer.  
XX XX  
XX PS Example 1; Page 13-20; 25pp; English.  
XX XX  
XX CC The present invention relates to a viral vector comprising first and  
XX CC second genes controlled by heterologous control elements, where the first  
XX CC gene is preferentially expressed in cells expressing human telomerase  
XX CC reverse transcriptase (hTERT), and another gene under the control of a  
XX CC heterologous transcriptional control element for a tissue or tumour  
XX CC specific gene other than TERT, and where transduction of the vector into  
XX CC a mammalian cell expressing TERT causes the death of the cell or its  
XX CC progeny. In particular, the second gene may be under the control of a  
XX CC transcriptional control element for a tissue specific gene selected from  
XX CC albumin, alpha-fetoprotein, prostate-specific antigen, mitochondrial  
XX CC creatine kinase, myelin basic protein, glial fibrillary acidic protein,  
XX CC and neuron-specific enolase. The second gene may be under the control of  
XX CC a transcriptional control element for a human telomerase RNA component  
XX CC (hTR). The vector of the invention is useful for killing a cancer cell,  
XX CC or treating a subject for a condition associated with increased  
XX CC expression of TERT in affected cells. The vector is also useful in the  
XX CC preparation of a medicament for treatment of a condition associated with  
XX CC increased expression of TERT, particularly cancer, and especially liver  
XX CC cancer, prostate cancer, muscle cancer, neural cell cancer, lung cancer,  
XX CC pancreatic cancer, medulloblastoma, cervical carcinoma, fibrosarcoma, and  
XX CC osteosarcoma. The present sequence represents a lambda clone  
XX CC (lambdaGphi5) containing human TERT DNA.  
XX XX  
XX SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;  
XX XX  
XX XX Query Match 100.0%; Score 1001; DB 10; Length 15418;  
XX XX Best Local Similarity 100.0%; Pred. No. 6.4e-291;  
XX XX Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX XX

Qy	1	GCCTGGGATTACAGGCACCCGCCACCATGCCAGCTAAATTTTTTGTGTAATTTTTAGTAGAGA	60
Dp	11500	GCCTGGGATTACAGGCACCCGCCACCATGCCAGCTAAATTTTTTGTGTAATTTTTAGTAGAGA	11559

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Qy 61 CGGGGTGGGGTGGGTTTCCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA 120
Db 11560 CGGGGTGGGGTGGGTTTCCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA 11619
Qy 121 TGATCCACCTGCTCTGCTCCCTTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCCA 180
Db 11620 TGATCCACCTGCTCTGCTCCCTTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCCA 11679
Qy 181 GCTCAGAAATTTACTCTGTTTAGAAAACATCTGGGTCTGAGGTGAGGAAGCTCACCCCACTCA 240
Db 11680 GCTCAGAAATTTACTCTGTTTAGAAAACATCTGGGTCTGAGGTGAGGAAGCTCACCCCACTCA 11739
Qy 241 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTTTATTTGTTTGTAGAACACTCTTGA 300
Db 11740 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTTTATTTGTTTGTAGAACACTCTTGA 11799
Qy 301 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCAACCC 360
Db 11800 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCAACCC 11859
Qy 361 ATAATACCTGGGTGTCTTCTGGGTATCAGCATCTTCAATTGAATGCGGAGGCGTTTCC 420
Db 11860 ATAATACCTGGGTGTCTTCTGGGTATCAGCATCTTCAATTGAATGCGGAGGCGTTTCC 11919
Qy 421 TCGCCATGCACATGGTGTGTTAACTACTCCAGCATAACTCTGCTTCCATTTCTTCTTTC 480
Db 11920 TCGCCATGCACATGGTGTGTTAACTACTCCAGCATAACTCTGCTTCCATTTCTTCTTTC 11979
Qy 481 CCTCTTTTAAATATGTTTCTATGTTGGCTTCTGCGAGAGAACAGGTAAAGCTACATA 540
Db 11980 CCTCTTTTAAATATGTTTCTATGTTGGCTTCTGCGAGAGAACAGGTAAAGCTACATA 12039
Qy 541 ACTTAACCTTTGTTGGAAACAAATTTTCCAAACCGCCCTTTGGCTTAGTGCGCAGACAA 600
Db 12040 ACTTAACCTTTGTTGGAAACAAATTTTCCAAACCGCCCTTTGGCTTAGTGCGCAGACAA 12099
Qy 601 TTCAAAACACAGCCCTTTAAAGGCTTAGGATGCTAAGGGGATTTCTAGAGAGCG 660
Db 12100 TTCAAAACACAGCCCTTTAAAGGCTTAGGATGCTAAGGGGATTTCTAGAGAGCG 12159
Qy 661 ACCGTAATCTTAAGTATTTACAGACGAGCTAACTCCAGCGAGGCTGACAGCCGAGG 720
Db 12160 ACCGTAATCTTAAGTATTTACAGACGAGCTAACTCCAGCGAGGCTGACAGCCGAGG 12219
Qy 721 GAGGTCGAGGCTGTTTCAAAATGCTAGCTCCATAAATAAGCAATTTCTCCGGCAGTT 780
Db 12220 GAGGTCGAGGCTGTTTCAAAATGCTAGCTCCATAAATAAGCAATTTCTCCGGCAGTT 12279
Qy 781 TCTGAAAGTAGGAAGGTTACATTTAAGGTTGCGTTTGTAGCAATTTCACTGTTTGCCTGA 840
Db 12280 TCTGAAAGTAGGAAGGTTACATTTAAGGTTGCGTTTGTAGCAATTTCACTGTTTGCCTGA 12339
Qy 841 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAGTTTCTCGCCCTTAGAT 900
Db 12340 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAGTTTCTCGCCCTTAGAT 12399
Qy 901 CCAAACTTGAGCAACCCGGAGTCTGGATTCCTGGGAAGTCTCTCAGCTGTCTCGGGTGT 960
Db 12400 CCAAACTTGAGCAACCCGGAGTCTGGATTCCTGGGAAGTCTCTCAGCTGTCTCGGGTGT 12459
Qy 961 GCCGGGGCCCGAGTCTGGAGGGACCAAGTGGCCGTGTGGC 1001
Db 12460 GCCGGGGCCCGAGTCTGGAGGGACCAAGTGGCCGTGTGGC 12500
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RESULT 6  
AAH41091  
ID AAH41091 standard; DNA; 3962 BP.  
XX  
AC AAH41091;  
XX  
DT 29-AUG-2001 (first entry)

```
XX  
DE  
XX  
KW Phenotype switch molecule; phenotype-related gene battery;  
KW gene localisation; telomere reverse transcriptase; TERT; ds.  
XX  
OS Unidentified.  
XX  
PN WO200138515-A1.  
XX  
XX 31-MAY-2001.  
XX  
PF 17-NOV-2000; 2000WO-CN000427.  
XX  
XX 19-NOV-1999; 99CN-00121466.  
XX  
PA (BIAN/) BIAN X.  
XX  
PI Bian X;  
XX  
DR WPI; 2001-367684/38.  
XX  
CC This invention relates to a method for isolating phenotype switch  
CC molecules and phenotype-related gene batteries from complex genomes of  
CC higher animals and plants. The method is useful in gene localisation and  
CC classification analysis, studying gene development networks and function  
CC networks, and designing drugs based on regulatory sequences of the  
CC phenotypes for disease treatment. The present sequence represents DNA  
CC encoding a telomere reverse transcriptase (TERT), which is used in an  
CC example illustrating the use of the method of the invention  
XX  
SQ Sequence 3962 BP; 782 A; 1157 C; 1113 G; 910 T; 0 U; 0 Other;  
  
Query Match 98.8%; Score 989; DB 4; Length 3962;  
Best Local Similarity 99.9%; Pred. No. 1.4e-287;  
Matches 1000; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
Qy 1 GGCTGGGATTTACAGGCACCGCCACCATGCTGGCTGCTCGAACTTCTGACCTCAGA 60  
Db 1882 GGCTGGGATTTACAGGCACCGCCACCATGCTGGCTGCTCGAACTTCTGACCTCAGA 1941  
Qy 61 CGGGGTGGGGTGGGTTTCCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA 120  
Db 1942 CGGGGTGGGGTGGGTTTCCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA 2001  
Qy 121 TGATCCACCTGCTCTGCTCCCTTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCCA 180  
Db 2002 TGATCCACCTGCTCTGCTCCCTTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCCA 2061  
Qy 181 GCTCAGAAATTTACTCTGTTTAGAAAACATCTGGGTCTGAGGTGAGGAAGCTCACCCCACTCA 240  
Db 2062 GCTCAGAAATTTACTCTGTTT- GAAACATCTGGGTCTGAGGTGAGGAAGCTCACCCCACTCA 2120  
Qy 241 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTTTATTTGTTTGTAGAACACTCTTGA 300  
Db 2121 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTTTATTTGTTTGTAGAACACTCTTGA 2180  
Qy 301 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCAACCC 360  
Db 2181 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCAACCC 2240  
Qy 361 ATAATACCTGGGTGTCTTCTGGGTATCAGCATCTTCAATTGAATGCGGAGGCGTTTCC 420  
Db 2241 ATAATACCTGGGTGTCTTCTGGGTATCAGCATCTTCAATTGAATGCGGAGGCGTTTCC 2300  
Qy 421 TCGCCATGCACATGGTGTGTTAACTACTCCAGCATAACTCTGCTTCCATTTCTTCTTTC 480
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Db 2301 TCGCCATGCACATGGTGTAAATTACTCCAGCATAACTCTCTGCTCCCAATTTCTTCTCTC 2360  
Qy CCTCTTTTAAATATGTTTCTATGTTGGCTTCTCTGCAGAGAACAGTGTAGCTACA 540  
Db CCTCTTTTAAATATGTTTCTATGTTGGCTTCTCTGCAGAGAACAGTGTAGCTACA 2420  
Qy ACTTAACCTTTTGTGGACAAATTTTCCAAACCGCCCTTTGCCCTAGTGCAGACAA 600  
Db ACTTAACCTTTTGTGGACAAATTTTCCAAACCGCCCTTTGCCCTAGTGCAGACAA 2480  
Qy TTCAACAACACAGCCCTTTAAAGGCTTAGGATCACTAAGGGATTTCTAGAGAGCG 660  
Db TTCAACAACACAGCCCTTTAAAGGCTTAGGATCACTAAGGGATTTCTAGAGAGCG 2540  
Qy ACCGTAATCTTAAGTATTCAAGACGAGGCTTAACCTCCAGCGAGGCTGACGCCAGG 720  
Db ACCGTAATCTTAAGTATTCAAGACGAGGCTTAACCTCCAGCGAGGCTGACGCCAGG 2600  
Qy GAGGCTGCGAGGCTTTCAATGCTAGCTCCATAAATAAAGCAATTTCTCCGCGAGTT 780  
Db GAGGCTGCGAGGCTTTCAATGCTAGCTCCATAAATAAAGCAATTTCTCCGCGAGTT 2660  
Qy TCTGAAGTAGGAAGGTTACATTAAGTTGCGTTGTTAGCAATTTCAAGTTTGCGGA 840  
Db TCTGAAGTAGGAAGGTTACATTAAGTTGCGTTGTTAGCAATTTCAAGTTTGCGGA 2720  
Qy CCTCAGCTACAGCATCCTCGAAGGCTTCGAGGACCCAGAGTTCTCGCCCTTAGAT 900  
Db CCTCAGCTACAGCATCCTCGAAGGCTTCGAGGACCCAGAGTTCTCGCCCTTAGAT 2780  
Qy CCAAACTTGAGCAACCCGAGTCTGGATTCTCTGGAAGTCTCTCAGCTGTCTCGGTTGT 960  
Db CCAAACTTGAGCAACCCGAGTCTGGATTCTCTGGAAGTCTCTCAGCTGTCTCGGTTGT 2840  
Qy GCCGGGCCCCAGGCTCGAGGGACACAGTGGCCGTGTGGC 1001  
Db GCCGGGCCCCAGGCTCGAGGGACACAGTGGCCGTGTGGC 2881

RESULT 7  
ID ADU82633 standard; DNA; 4356 BP.  
XX AC ADU82633;  
XX 10-FEB-2005 (first entry)  
DE Human hTERT gene nucleotide sequence.  
XX Gene expression; transcription; TERT; telomerase reverse transcriptase;  
KW cancer therapy; cytostatic; CNS; respiratory; anti-HIV; antianemic;  
KW antisickling; hemostatic; antidiabetic; cardiant; antiinflammatory;  
KW antirheumatic; antiarthritic; neuroprotective; antiasthmatic; vasotropic;  
KW gene therapy; apoptosis stimulator; cancer; gene; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 3997..4215  
CDS /\*tag= a  
FT /\*product= "telomerase reverse transcriptase fragment"  
FT /\*partial  
XX  
XX WO2004099377-A2.  
XX  
XX 18-NOV-2004.  
XX  
XX 30-APR-2004; 2004WO-US013487.  
XX  
XX 01-MAY-2003; 2003US-0467171P.  
XX  
XX (MUSC-) MUSC FOUND RES DEV.  
XX

PI Dong J, Rubinchik S, Woratanadham J;  
XX WPI: 2004-8051118/79.  
DR P-PSDB: ADU82634.  
DR GENBANK: AF097365.  
XX  
PT New expression vector comprising a first expression cassette with a first  
PT coding region that encodes a transcriptional activating factor (TAP),  
PT useful in treating cancer, AIDS, hemophilia, diabetes and asthma.  
XX  
XX Disclosure; SEQ ID NO 5; 112pp; English.  
XX  
XX The invention relates to an expression vector comprising a first  
XX expression cassette having a first coding region that encodes a  
XX transcriptional activating factor (TAP), and a second expression cassette  
XX comprising a second coding region that encodes a selected polypeptide.  
XX The expression vector further comprises a first expression cassette  
XX having a first coding region that encodes a transcriptional activating  
XX factor (TAP), the first coding region being positioned under the  
XX transcriptional control of a first promoter comprising a tissue specific  
XX regulatory element (TSRE), and a TAP binding site (TBS), and a second  
XX expression cassette comprising a second coding region that encodes a  
XX selected polypeptide, the second coding region being positioned under the  
XX transcriptional control of a second promoter comprising a TSRE and a TBS,  
XX or a TBS. The expression vector further comprises a third coding region  
XX that encodes a first transcriptional silencer (TSI), the third coding  
XX region being positioned under the transcriptional control, a third  
XX promoter comprising a TSRE and a TBS, and a fourth expression cassette  
XX comprising a fourth coding region that encodes a second TSI, the fourth  
XX coding region being positioned under the transcriptional control of a  
XX fourth promoter that is negatively regulated by the first TSI, where the  
XX first, second and third promoters are negatively regulated by the second  
XX TSI. The selected polypeptide is a therapeutic polypeptide, such as an  
XX anti-cancer polypeptide that is a tumor suppressor, and inducer of  
XX apoptosis, and cell cycle regulator, a toxin, or an inhibitor of  
XX angiogenesis, and an enzyme, a cytokine, a hormone, a tumor antigen, a  
XX human antigen or a pathogen antigen. The selected polypeptide is  
XX essential for vector replication, where the vector is an adenoviral  
XX vector. The expression vector is useful in methods for treating cancer  
XX and further comprises a selectable or screenable marker. The methods and  
XX compositions of the present invention are useful in the fields of  
XX molecular biology and gene therapy, particularly to the combined spatial  
XX and quantitative regulation of transgene expression in eukaryotic cells,  
XX and in treating cancer including breast cancer, ovarian cancer, fallopian  
XX tube cancer, cervical cancer, uterine cancer, prostate cancer, testicular  
XX cancer, pancreatic cancer, colon cancer, bladder cancer, liver cancer,  
XX stomach cancer, lung cancer, lymphoid cancer, brain cancer, thyroid  
XX cancer, head and neck cancer, skin cancer or leukemia. The cancer is a  
XX recurrent cancer, a metastatic cancer or a drug resistant cancer. The  
XX methods and compositions can also be used in treating cystic fibrosis,  
XX AIDS, sickle cell anemia, hemophilia, diabetes, heart disease,  
XX inflammatory disorders, rheumatoid arthritis, multiple sclerosis, asthma  
XX and restenosis. The present sequence represents a human telomerase  
XX reverse transcriptase (hTERT) gene nucleotide sequence, the promoter  
XX fragment can be used in the vectors of the invention.  
XX  
SQ Sequence 4356 BP; 829 A; 1298 C; 1254 G; 975 T; 0 U; 0 Other;  
Query Match 98.8%; Score 989; DB 13; Length 4356;  
Best Local Similarity 99.9%; Pred. No. 1.4e-287;  
Matches 1000; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
Qy 1 GGCTGGGATTACAGCACCACCCACCATGCGCCAGCTGCTCTCGAAGTCTTCGACCTCAGA 60  
Db 1953 GGCTGGGATTACAGCACCACCCACCATGCGCCAGCTGCTCTCGAAGTCTTCGACCTCAGA 2012  
Qy 61 CGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTTCGAACCTTCGACCTCAGA 120  
Db 2013 CGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTTCGAACCTTCGACCTCAGA 2072  
Qy 121 TGATCCACCTGCCTCTGCCTCCTAAAGTGTGGGATTACAGGTGTGACCCACCATGCCCA 180  
Db 2073 TGATCCACCTGCCTCTGCCTCCTAAAGTGTGGGATTACAGGTGTGACCCACCATGCCCA 2132

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QY 181 GCTCAGAAATTAATCTCTGTTAGAAACATCTGGCTCTGAGTAGAGAGCTCACCCCACTCA 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2133 GCTCAGAAATTAATCTCTGTTT- GAACAACATCTGGGCTGAGGTAGGAAGCTCACCCCACTCA 2191
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 AGTGTGTGTGTGTTTAAAGCAATGATAGAAATTTTATTTATTTGTTAGAACACTCTTTGA 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2192 AGTGTGTGTGTGTTTAAAGCAATGATAGAAATTTTATTTATTTGTTAGAACACTCTTTGA 2251
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 TGTTTTACATCTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCAACC 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2252 TGTTTTACATCTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCAACC 2311
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 361 ATAATCTGGGGTGTCTTCTGGGTATCAGGATCTTCATTTGAATCCGGGAGGGTTTCC 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2312 ATAATCTGGGGTGTCTTCTGGGTATCAGGATCTTCATTTGAATCCGGGAGGGTTTCC 2371
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 421 TCGCCATGACATGGTGTAAATTAATCTCAGCATAACTTCTGCTTCCATTTCTTCTTTC 480
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2372 TCGCCATGACATGGTGTAAATTAATCTCAGCATAACTTCTGCTTCCATTTCTTCTTTC 2431
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 481 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTTCGACAGAAACAGTGTAAAGTACA 540
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2432 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTTCGACAGAAACAGTGTAAAGTACA 2491
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 541 ACTTAACCTTTTGTGGAAACAAATTTCCAAACCGCCCTTGGCCCTAGTGGCAGAGCAA 600
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2492 ACTTAACCTTTTGTGGAAACAAATTTCCAAACCGCCCTTGGCCCTAGTGGCAGAGCAA 2551
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 601 TTCACAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAGAGCG 660
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2552 TTCACAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAGAGCG 2611
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 661 ACCGTAATCCTAAGTATTACAAAGCAGGCTAACCTCAGCGAGGTCACAGCCGAG 720
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QY 2612 ACCGTAATCCTAAGTATTACAAAGCAGGCTAACCTCAGCGAGGTCACAGCCGAG 2671
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 721 GAGGTGCGAGGCTGTTCAAATGCTAGCTCCATTAATAAGCAATTTCTCCGGCAGTT 780
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2672 GAGGTGCGAGGCTGTTCAAATGCTAGCTCCATTAATAAGCAATTTCTCCGGCAGTT 2731
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 781 TCTGAAAGTAGGAAAGGTATACATTTAAGTTGCGTTTGTAGCATTTTCAGTGTTCGCCGA 840
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2732 TCTGAAAGTAGGAAAGGTATACATTTAAGTTGCGTTTGTAGCATTTTCAGTGTTCGCCGA 2791
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 841 CCTCAGCTACAGCATCCCTCAAGGCTCTCGGAGACCCAGAGTTTCTCGCCCTTAGAT 900
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2792 CCTCAGCTACAGCATCCCTCAAGGCTCTCGGAGACCCAGAGTTTCTCGCCCTTAGAT 2851
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 901 CCAAACTTGAGCAACCCGGAGTCTGGATTCTTGGGAAGTCTCAGCTGTCTCGGTTGT 960
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2852 CCAAACTTGAGCAACCCGGAGTCTGGATTCTTGGGAAGTCTCAGCTGTCTCGGTTGT 2911
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 961 GCCGGGGCCCCAGGTCTGGAGGGGACCCAGTGGCCGTGTGGC 1001
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2912 GCCGGGGCCCCAGGTCTGGAGGGGACCCAGTGGCCGTGTGGC 2952
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

## RESULT 8

ADV23865

ID ADV23865 standard; DNA; 4293 BP.

AC ADV23865;

XX 24-FEB-2005 (first entry)

XX Human hTERT gene 5' flanking region, intron 1 and exon 1, SEQ ID 1.

XX Cytostatic; Gene therapy; cancer; telomerase;

XX telomerase reverse transcriptase; hTERT; enzyme; gene; ds.

XX Homo sapiens.

XX

	Key	Location/Qualifiers
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FT		/tag= a
FT		/note= "This region is specifically claimed in Claims 4 and 15"
FT	misc_feature	2251..3920
FT		/tag= b
FT		/note= "This region is specifically claimed in Claims 4 and 15"
FT	misc_feature	2791..3955
FT		/tag= c
FT		/note= "This region is specifically claimed in Claims 4 and 15"
FT	misc_feature	2967..3955
FT		/tag= d
FT		/note= "This region is specifically claimed in Claims 4 and 15"
FT	misc_feature	3531..3955
FT		/tag= e
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FT	misc_feature	3545..3609
FT		/tag= f
FT		/note= "This region is identical to the Hepatitis B virus (HBV) integration site in the huH-4 cell line"
FT	misc_feature	3612..3955
FT		/tag= g
FT		/note= "This region is specifically claimed in Claims 4 and 15"
FT	misc_feature	3661..3955
FT		/tag= h
FT		/note= "This region is specifically claimed in Claims 4 and 15"
FT	misc_feature	3705..3955
FT		/tag= i
FT		/note= "This region is specifically claimed in Claims 4 and 15"
FT	misc_feature	3708..3766
FT		/tag= j
FT		/note= "This region is responsible for full promoter activity"
FT	misc_feature	3729..3734
FT		/tag= k
FT		/note= "Upstream E-box"
FT	misc_feature	3828..3955
FT		/tag= l
FT		/note= "This region is specifically claimed in Claims 4 and 15"
FT	misc_feature	3883..3955
FT		/tag= m
FT		/note= "This region is specifically claimed in Claims 4, 15, 19 and 20"
FT	5'UTR	3916..3970
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FT	primer_bind	4029..4050
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FT	intron	4190..4293
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FT		/number= 1
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XX		US2004248246-A1.
XX		

PD 09-DEC-2004.  
XX  
XX  
XX 05-JUN-2003; 2003US-00456830.  
XX  
XX 05-JUN-2003; 2003US-00456830.  
XX  
XX (USAS ) NASA US NAT AERO & SPACE ADMIN.  
XX  
XX Horikawa I, Barrett JC;  
XX  
XX WPI; 2005-020562/02.  
XX P-PSDB; ADV23866.  
XX  
XX New regulatory control sequence comprising a promoter that directs  
XX differential expression of an operably linked heterologous nucleic acid  
XX sequence in a first cell type, useful for preparing a composition for  
XX treating cancer.  
XX  
XX Claim 4; SEQ ID NO 1; 46pp; English.  
XX  
XX The present invention relates to a new regulatory control sequence (I)  
XX which is useful for preparing a composition for treating cancer. (I)  
XX comprises: (a) a promoter that directs differential expression of an  
XX operably linked heterologous nucleic acid sequence (e.g. cytotoxins) in a  
XX first cell type as compared to a second cell type, where the first cell  
XX type is a telomerase-positive or a cancer cell and the second cell type  
XX is a telomerase-negative or a normal somatic cell; and (b) at least one  
XX exogenous E-box element linked in cis with the promoter sequence and that  
XX enhances the differential expression directed by the promoter. The  
XX promoter is preferably an human telomerase reverse transcriptase (hTERT)  
XX promoter. hTERT is the catalytic subunit of the human telomerase complex,  
XX which is responsible for the replication of telomeres. E-box elements are  
XX regulatory control elements that are recognized by numerous transcription  
XX factors, e.g. transcription factors from the basic helix-loop-helix  
XX structural family. Differential E-box-mediated repression of hTERT gene  
XX promoter activity has been discovered, where repression occurs in normal  
XX cells but not in many cancer cells. By linking E-box elements in cis with  
XX TERT transcriptional regulatory sequences, the expression of heterologous  
XX sequences operably linked to the TERT transcriptional regulatory  
XX sequences, can be preferentially suppressed in normal cells. However, the  
XX expression of such heterologous sequences is not suppressed in cancer  
XX cells. The present sequence is the nucleotide sequence in the 5'-flanking  
XX region, exon 1 and intron 1 of the hTERT gene, used to illustrate the  
XX invention.  
XX  
XX Sequence 4293 BP; 817 A; 1278 C; 1234 G; 961 T; 0 U; 3 Other;

Query Match 98.8%; Score 988.6; DB 14; Length 4293;  
Best Local Similarity 99.8%; Pred. No. 1.9e-287;  
Matches 999; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
QY 1 GCCTGGGATTACAGGACCGCCACATGCCAGCTAATTTTGTATTTTAGTAGAGA 60  
DB 1927 GCGTGGGATTACAGGACCGCCACATGCCAGCTAATTTTGTATTTTAGTAGAGA 1986  
QY 61 CGGGGGTGGGGTGGGGTTCACATGTTGGCCAGCTGCTCGAATTTCTGACCTCAGA 120  
DB 1987 CGGGGGTGGGGTGGGGTTCACATGTTGGCCAGCTGCTCGAATTTCTGACCTCAGA 2046  
QY 121 TGATCCACTGCTCTGCTCTCCTAAAGTCTGGGATTACAGGTGAGCCACCATGCCA 180  
DB 2047 TGATCCACTGCTCTGCTCTCCTAAAGTCTGGGATTACAGGTGAGCCACCATGCCA 2106  
QY 181 GCTCAGAAATTTACTCTGTTTAAAGACATCTGGGTCTGAGGTAGGAGCTCACCCACTCA 240  
DB 2107 GCTCAGAAATTTACTCTGTTT-AAAGACATCTGGGTCTGAGGTAGGAGCTCACCCACTCA 2165  
QY 241 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTCTGTAGACACTCTGA 300  
DB 2166 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTCTGTAGACACTCTGA 2225  
QY 301 TGTTTTACACTCTGATGACTAGACATCATCAGCTTTTCAAAGACACACTAATCTCACCC 360

DB 2226 TGTTTTACACTCTGATGACTAGACATCATCAGCTTTTCAAAGACACACTAATCTCACCC 2285  
QY 361 ATAATACCTGGGGTGTCTTCTGGGTATCAGCGATCTTCAATGAATCCCGGAGGGTTC 420  
DB 2286 ATAATACCTGGGGTGTCTTCTGGGTATCAGCGATCTTCAATGAATCCCGGAGGGTTC 2345  
QY 421 TCGCCATGCAACATGGTGTAAATTAATCTCAGCATTAATCTTCTGCTTCATTTCTTCTTC 480  
DB 2346 TCGCCATGCAACATGGTGTAAATTAATCTCAGCATTAATCTTCTGCTTCATTTCTTCTTC 2405  
QY 481 CCTCTTTTAAATTTGTTTCTATGTTGGCTCTCTGCAGAGAACCACTGTAAGCTACA 540  
DB 2406 CCTCTTTTAAATTTGTTTCTATGTTGGCTCTCTGCAGAGAACCACTGTAAGCTACA 2465  
QY 541 ACTTAACTTTTGTGGAAACAAATTTTCAAACCGCCCTTTGGCCCTAGTGCAGAGACAA 600  
DB 2466 ACTTAACTTTTGTGGAAACAAATTTTCAAACCGCCCTTTGGCCCTAGTGCAGAGACAA 2525  
QY 601 TTCAAAACACAGCCCTTTTAAAGGCTTAAAGGATCACTAAGGGGATTTCTAGAAAGCGG 660  
DB 2526 TTCAAAACACAGCCCTTTTAAAGGCTTAAAGGATCACTAAGGGGATTTCTAGAAAGCGG 2585  
QY 661 ACCGTAATCTTAAGTATTTTACAGAGCAGGCTAACTCCAGCGCGGTGACAGCCAGG 720  
DB 2586 ACCGTAATCTTAAGTATTTTACAGAGCAGGCTAACTCCAGCGCGGTGACAGCCAGG 2645  
QY 721 GAGGTCGCGGCTGTTTCAATGCTAGCTCCATAAATAAAGCAATTTCTCCGCGAGTT 780  
DB 2646 GAGGTCGCGGCTGTTTCAATGCTAGCTCCATAAATAAAGCAATTTCTCCGCGAGTT 2705  
QY 781 TCTGAAAGTAGGAAAGGTTTACATTTAAGGTTGCGTTTGTAGCAATTTCTGCTTCGCG 840  
DB 2706 TCTGAAAGTAGGAAAGGTTTACATTTAAGGTTGCGTTTGTAGCAATTTCTGCTTCGCG 2765  
QY 841 CCTCAGCTACAGCATCTCTGCAAGGCTTCGGAGACCCAGAGTTTCTGCGCCCTTAGAT 900  
DB 2766 CCTCAGCTACAGCATCTCTGCAAGGCTTCGGAGACCCAGAGTTTCTGCGCCCTTAGAT 2825  
QY 901 CCAAACTTGAGCAACCCGAGTCTGGATTCTCTGGGAGTCTCTCAGCTGCTCTGCGGTTGT 960  
DB 2826 CCAAACTTGAGCAACCCGAGTCTGGATTCTCTGGGAGTCTCTCAGCTGCTCTGCGGTTGT 2885  
QY 961 GCCGGGGCCCCAGGCTTGGAGGGGACCACTGTCGCGGTGTGGC 1001  
DB 2886 GCCGGGGCCCCAGGCTTGGAGGGGACCACTGTCGCGGTGTGGC 2926

RESULT 9  
ADU82631  
ID ADU82631 standard; DNA; 5491 BP.  
XX  
AC ADU82631;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
XX Human hTERT gene nucleotide sequence.  
XX  
DB Gene expression; transcription; TERT; telomerase reverse transcriptase;  
XX cancer therapy; cytostatic; CNS; respiratory; anti-HIV; antineoplastic;  
XX antiskilling; hemostatic; antidiabetic; cardiac; antinflammatory;  
XX antirheumatic; antithrombotic; neuroprotective; antiaesthetic; vasotropic;  
XX gene therapy; apoptosis stimulator; cancer; gene; ds.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX CDS 3415..3633  
XX FT /\*tag= a  
XX FT /product= "telomerase reverse transcriptase fragment"  
XX FT /partial  
XX  
XX WO2004099377-A2.







XX DE DNA encoding human telomerase reverse transcriptase (TERT) #1.  
XX XX  
KW Telomerase reverse transcriptase; TERT; cytosolic; apoptosis;  
KW cell growth inhibitor; antisense oligonucleotide; antisense technology;  
KW ds.  
XX OS Homo sapiens.  
XX XX  
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FT exon 1. .11492  
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FT /\*tag= b  
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FT /note= "Telomerase reverse transcriptase"  
FT intron 11493. .11596  
FT /\*tag= c  
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FT 11597. .12950  
FT /\*tag= d  
FT /number= 2  
FT 12951. .21566  
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XX WO200188198-A1.  
XX PN  
XX 22-NOV-2001.  
XX PD  
XX 15-MAY-2001; 2001WO-US015774.  
XX PF  
XX 16-MAY-2000; 2000US-00572423.  
XX PR  
XX 07-DEC-2000; 2000US-00733294.  
XX PA (ISIS-) ISIS PHARM INC.  
XX XX  
FI Monia BP, Gaarde WA, Freier SM, Wanciewicz B;  
XX WPI; 2002-075321/10.  
XX P-PSDB; AAU72735.  
XX DR  
XX  
XX New compound targeted to nucleic acid molecule encoding telomerase  
FT transcriptase (TERT), which specifically hybridizes with and inhibits  
FT expression of TERT, useful for modulating apoptosis and inhibiting cell  
FT growth.  
XX  
PS Example 19; Page 112-138; 154pp; English.  
XX  
XX The invention describes a compound, 8-50 nucleobases in length targeted  
CC to a nucleic acid molecule encoding human TERT (telomerase reverse  
CC transcriptase), where the compound specifically hybridizes with and  
CC inhibits the expression of TERT. A series of oligonucleotides were  
CC designed to target different regions of a central gap region consisting of  
CC nucleotides in length and composed of ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by  
CC five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-  
CC MOE) nucleotides. The compounds were analysed for their effect on human  
CC TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction  
CC (PCR). The compound is useful for inhibiting the expression of TERT in  
CC cells or tissues, for treating a human having disease or condition  
CC associated with TERT, for modulating apoptosis, for inhibiting cell  
CC growth (preferably, cancer cell growth), in antisense therapy and for  
CC diagnostics and therapeutics. This sequence encodes human telomerase

CC reverse transcriptase (TERT) #1, and is used to create antisense  
CC oligonucleotides which modify TERT expression, described in the method of  
CC the invention

XX Sequence 5152 BP; 10709 A; 13313 C; 15370 G; 12158 T; 0 U; 2 Other;

Query Match 97.2%; Score 972.8; DB 6; Length 5152;  
Best Local Similarity 99.5%; Pred. No. 3.9e-282;  
Matches 997; Conservative 0; Mismatches 2; Indels 3; Gaps 2;  
Qy 1 GGCTGGGAATTACAGGACACCGCCACCATGCGCAGCTAATTTTGTATTTTGTAGTAGAGA 60  
Db 9230 GGCTGGGAATTACAGGACACCGCCACCATGCGCAGCTAATTTTGTATTTTGTAGTAGAGA 9289  
Qy 61 CGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAATTTCTGACCTCAGA 120  
Db 9290 CGGGGGT- -GGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAATTTCTGACCTCAGA 9347  
Qy 121 TGATCCACCTGCTCTGCTTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCCA 180  
Db 9348 TGATCCACCTGCTCTGCTTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCCA 9407  
Qy 181 GCTCAGAAATTACTCTGTTTAGAAACATCTGGGTCTCAGGTGAGAACTCACCCCACTCA 240  
Db 9408 GCTCAGAAATTACTCTGTTTAGAAACATCTGGGTCTCAGGTGAGAACTCACCCCACTCA 9467  
Qy 241 AGTGTGTGGTGTGTTTAAAGCCATGATAGAAATTTTATTTTGTGTAGAACACTCTTGA 300  
Db 9468 AGTGTGTGGTGTGTTTAAAGCCATGATAGAAATTTTATTTTGTGTAGAACACTCTTGA 9527  
Qy 301 TGTTTACATGTCATGACATAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360  
Db 9528 TGTTTACATGTCATGACATAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 9587  
Qy 361 ATAATCTGGGGTCTCTTGGGTATCAGGATCTTCATTGAATGCGGGAGGGTTC 420  
Db 9588 ATAATCTGGGGTCTCTTGGGTATCAGGATCTTCATTGAATGCGGGAGGGTTC 9647  
Qy 421 TCGCCATGCATGGTGTAAATTAATCTCAGCAATCTCTGCTTCCATTTCTCTCTTC 480  
Db 9648 TCGCCATGCATGGTGTAAATTAATCTCAGCAATCTCTGCTTCCATTTCTCTCTTC 9707  
Qy 481 CCTCTTTTAAATGTGTTTCTATGTTGGCTCTCTGCAGAAACAGTGTAGTACACA 540  
Db 9708 CCTCTTTTAAATGTGTTTCTATGTTGGCTCTCTGCAGAAACAGTGTAGTACACA 9767  
Qy 541 ACTTAACTTTTGTGGACAAATTTTCCAAACCGCCCTTTGCCCTAGTGCAGAGCAA 600  
Db 9768 ACTTAACTTTTGTGGACAAATTTTCCAAACCGCCCTTTGCCCTAGTGCAGAGCAA 9827  
Qy 601 TTCAAAACACAGCCCTTTAAAGGCTTAGGATCACTAAGGGATTTCTAGAGAGCG 660  
Db 9828 TTCAAAACACAGCCCTTTAAAGGCTTAGGATCACTAAGGGATTTCTAGAGAGCG 9887  
Qy 661 ACCGTAATCTTAAGTATTTTACAAGACAGGCTTAACCTCCAGCGAGGTGCACGCCAGG 720  
Db 9888 ACCGTAATCTTAAGTATTTTACAAGACAGGCTTAACCTCCAGCGAGGTGCACGCCAGG 9947  
Qy 721 GAGGGTCGAGGCCCTGTTTCAAATGCTAGCTCCATAAATAAGCAATTTTCTCCGCGAGTT 780  
Db 9948 GAGGGTCGAGGCCCTGTTTCAAATGCTAGCTCCATAAATAAGCAATTTTCTCCGCGAGTT 10007  
Qy 781 TCTGAAAGTAGAAAGGTTTACATTTAAGTGTGGTGTGTTGTAGCATTTTCAGTGTTCGGA 840  
Db 10008 TCTGAAAGTAGAAAGGTTTACATTTAAGTGTGGTGTGTTGTAGCATTTTCAGTGTTCGGA 10067  
Qy 841 CCTCAGCTACAGCATCCTCGAAGCCCTCGGGAGACCCAGAAAGTTTCTCG-CCCTTTAGA 899  
Db 10068 CCTCAGCTACAGCATCCTCGAAGCCCTCGGGAGACCCAGAAAGTTTCTCGCCCCCTTAGA 10127  
Qy 900 TCCAAACTTGAGCAACCGGAGTCTGGAATTCCTCGGAGTCTCCTCAGCTGCTCCTCGGTTG 959  
Db 10128 TCCAAACTTGAGCAACCGGAGTCTGGAATTCCTCGGAGTCTCCTCAGCTGCTCCTCGGTTG 10187

Qy 960 TGCCGGGGCCCCCAGGCTCTGAGGGGACCACTGGCCGCTGTGGC 1001  
Db 10188 TGCCGGGGCCCCCAGGCTCTGAGGGGACCACTGGCCGCTGTGGC 10229

## RESULT 11

AA88272  
ID AAX88272 standard; DNA; 5126 BP.

XX AAX88272;

DT 22-SEP-1999 (first entry)

XX Human catalytic telomerase subunit 5'-flanking regulatory DNA.

XX Telomerase; subunit; human; regulatory; catalytic; anti-tumour; reporter;  
KW modulator; telomerase regulatory region; cancer therapy; ss.

XX Homo sapiens.

XX DE19757984-A1.

XX 01-JUL-1999.

XX 24-DEC-1997; 97DE-01057984.

XX 24-DEC-1997; 97DE-01057984.

XX (FARB ) BAYER AG.

XX Hagen G, Wick M, Zubov D;

XX WPI; 1999-372320/32.

XX New 5' flanking regulatory sequence from the human catalytic telomerase  
PT subunit gene useful for cancer therapy.

XX Claim 1; Fig 4; 14pp; German.

XX This invention describes a novel 5' flanking regulatory sequence from the  
CC human catalytic telomerase subunit gene. Recombinant constructs  
CC containing the product of the invention can be linked with DNA encoding  
CC an anti-tumour protein or reporter protein. The constructs are useful for  
CC identifying candidate substances that modulate the activity of the  
CC telomerase regulatory region. The constructs can be used in cancer  
CC therapy

XX Sequence 5126 BP; 1009 A; 1532 C; 1404 G; 1180 T; 0 U; 1 Other;

Query Match 97.1%; Score 971.8; DB 2; Length 5126;  
Best Local Similarity 99.4%; Pred. No. 2.4e-282;  
Matches 996; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

Qy 1 GGCTGGGAATTACAGGACACCGCCACCATGCGCAGCTAATTTTGTATTTTGTAGTAGAGA 60  
Db 3080 GGCTGGGAATTACAGGACACCGCCACCATGCGCAGCTAATTTTGTATTTTGTAGTAGAGA 3139

Qy 61 CGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAATTTCTGACCTCAGA 120  
Db 3140 CGGGGGT- -GGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAATTTCTGACCTCAGA 3197

Qy 121 TGATCCACCTGCTCTGCTTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCCA 180  
Db 3198 TGATCCACCTGCTCTGCTTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCCA 3257

Qy 181 GCTCAGAAATTACTCTGTTTAGAAACATCTGGGTCTCAGGTAGGAAGCTCACCCCACTCA 240  
Db 3258 GCTCAGAAATTACTCTGTTTAGAAACATCTGGGTCTCAGGTAGGAAGCTCACCCCACTCA 3317

Qy 241 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTGTGTGTAGAACTCTTGA 300  
Db 3318 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTGTGTGTAGAACTCTTGA 3377



Db 2021 CCAAGTGAAGCTACAACTTAACCTTTTGTGTGAACAAATTTTCCAAACCGGCCCTTTGGCC 1962  
Qy 586 TAGTGGCAGAGACAATTCACAAACACAGCCCTTTAAAGAGCTTAGGGATCACTTAAGGGG 645  
Db 1961 TAGTGGCAGAGACAATTCACAAACACAGCCCTTTAAAGAGCTTAGGGATCACTTAAGGGG 1902  
Qy 646 ATTTCTAGAGAGCGGCCGCTTAACCTTAAGTATTTTACAAGCAGAGGCTAACCTCCAGCGA 705  
Db 1901 ATTTCTAGAGAGCGGCCGCTTAACCTTAAGTATTTTACAAGCAGAGGCTAACCTCCAGCGA 1842  
Qy 706 GCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 765  
Db 1841 GCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1782  
Qy 766 TTTCTCCGCGAGTTTCTGAAAGTAGGAAGTTTACATTTAAAGTTGCGTTTGTAGCAT 825  
Db 1781 TTTCTCCGCGAGTTTCTGAAAGTAGGAAGTTTACATTTAAAGTTGCGTTTGTAGCAT 1722  
Qy 826 TTCAGTGTGTTCGAGCCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGAGCCCAAGAGTT 885  
Db 1721 TTCAGTGTGTTCGAGCCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGAGCCCAAGAGTT 1662  
Qy 886 TCTCGCCCTTTAGATCAAACTTGAGCAACCCGAGTCTGGATTCCTCGGAGAGTCCTCAG 945  
Db 1661 TCTCGCCCTTTAGATCAAACTTGAGCAACCCGAGTCTGGATTCCTCGGAGAGTCCTCAG 1602  
Qy 946 CTGTCCTGCGGTTGTGCGGGGCCCGAGGTCGAGGGGACCAAGTGCGCGGTGGG 1001  
Db 1601 CTGTCCTGCGGTTGTGCGGGGCCCGAGGTCGAGGGGACCAAGTGCGCGGTGGG 1546

## RESULT 13

AEAL8025/c  
ID AEAL8025 standard; DNA; 7928 BP.  
AC AEAL8025;  
XX  
DT 11-AUG-2005 (first entry)  
XX  
DE Human gynecological cell proliferative disorder gene SEQ ID NO 11.  
XX  
KW detection; prognosis; cell proliferative disorder; cervical cancer;  
KW endometrial cancer; neoplasia; cancer; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2005049861-A2.  
XX  
PD 02-JUN-2005.  
XX  
PF 10-NOV-2004; 2004WO-EP012740.  
XX  
PR 10-NOV-2003; 2003EP-00025739.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Widschwendter M;  
XX  
DR WPI; 2005-396129/40.  
XX  
PT Detecting, differentiating, and prognosing a gynecological cell  
PT proliferative disorder by obtaining a cervicovaginal secretion specimen  
PT from an individual and determining the methylation status of at least one  
PT or more CpG positions.  
XX  
PS Claim 3; SEQ ID NO 11; 163pp; English.  
XX  
CC The invention relates to a method of detecting, differentiating, and  
CC prognosing a gynecological cell proliferative disorder comprising  
CC obtaining a cervicovaginal secretion specimen from an individual,  
CC determining the methylation status of at least one or more CpG positions,  
CC and determining from the methylation status the presence, classification,  
CC and/or prognosis of a gynecological cell proliferative disorder in the

CC individual. The method is useful for detecting, differentiating, and  
CC prognosing a gynecological cell proliferative disorder, e.g. dysplasia or  
CC low-grade squamous intraepithelial lesions, high-grade squamous  
CC intraepithelial lesions, cervical cancer, endometrial cancer, or grade 1  
CC to 3 cervical intraepithelial neoplasia. The present sequence represents  
CC a human gynecological cell proliferative disorder related gene.

XX  
SQ Sequence 7928 BP; 1629 A; 2721 C; 2411 G; 1167 T; 0 U; 0 Other;  
Query Match 95.3%; Score 954.4; DB 14; Length 7928;  
Best Local Similarity 99.9%; Pred. No. 5.5e-277;  
Matches 955; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 46 TATTTTGTAGTACAGACGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGA 105  
Db 7928 TATTTTGTAGTACAGACGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGA 7869  
Qy 106 ACTTCTGACCTCAGATGATCCACTGCTCTGCTCTTAAAGTCTGGGATTAACAGGTGT 165  
Db 7868 ACTTCTGACCTCAGATGATCCACTGCTCTGCTCTTAAAGTCTGGGATTAACAGGTGT 7809  
Qy 166 GAGCCACCATGCCCAGCTCAGAAATTAATCTGTTTAAAGAAACATCTGGGTCTGAGGTAGGA 225  
Db 7808 GAGCCACCATGCCCAGCTCAGAAATTAATCTGTTTAAAGAAACATCTGGGTCTGAGGTAGGA 7749  
Qy 226 AGCTCACCCCACTCAAGTGTGGTGTAAAGCCAAATGATAGAAATTTTATTCTGTTG 285  
Db 7748 AGCTCACCCCACTCAAGTGTGGTGTAAAGCCAAATGATAGAAATTTTATTCTGTTG 7699  
Qy 286 TTAGAACACTCTTGATGTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGAC 345  
Db 7688 TTAGAACACTCTTGATGTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGAC 7629  
Qy 346 ACCTAACTGACCCCACTAATCTGGGTGTCTCTGGGTATCAGCGATCTTCAATGTAATG 405  
Db 7628 ACCTAACTGACCCCACTAATCTGGGTGTCTCTGGGTATCAGCGATCTTCAATGTAATG 7569  
Qy 406 CCGGAGGCGTTTCTCGCCATGACATGCTGTAAATTAATCTCCAGCATATCTCTGCTT 465  
Db 7568 CCGGAGGCGTTTCTCGCCATGACATGCTGTAAATTAATCTCCAGCATATCTCTGCTT 7509  
Qy 466 CCATTTCTCTCTCCCTCTTTTAAATTTCTATGTTGGCTTCTCTGACAGAGAA 525  
Db 7508 CCATTTCTCTCTCCCTCTTTTAAATTTCTATGTTGGCTTCTCTGACAGAGAA 7449  
Qy 526 CCAGTGAAGCTACAACTTAATCTTTTGGAAACAAATTTTCAAACCGGCCCTTTGCC 585  
Db 7448 CCAGTGAAGCTACAACTTAATCTTTTGGAAACAAATTTTCAAACCGGCCCTTTGCC 7389  
Qy 586 TAGTGGCAGAGACAATTCACAAACAGCCCTTTTAAAGAGCTTAGGGATCACTTAAGGGG 645  
Db 7388 TAGTGGCAGAGACAATTCACAAACAGCCCTTTTAAAGAGCTTAGGGATCACTTAAGGGG 7329  
Qy 646 ATTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 705  
Db 7328 ATTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7269  
Qy 706 GCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 765  
Db 7268 GCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7209  
Qy 766 TTTCTCCGCGAGTTTCTGAAAGTAGGAAGTTTACATTTAAAGTTGCGTTTGTAGCAT 825  
Db 7208 TTTCTCCGCGAGTTTCTGAAAGTAGGAAGTTTACATTTAAAGTTGCGTTTGTAGCAT 7149  
Qy 826 TTCAGTGTGTTCGAGCCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGAGCCCAAGAGTT 885  
Db 7148 TTCAGTGTGTTCGAGCCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGAGCCCAAGAGTT 7089  
Qy 886 TCTCGCCCTTTAGATCAAACTTGAGCAACCCGAGTCTGGATTCCTCGGAGAGTCCTCAG 945  
Db 7088 TCTCGCCCTTTAGATCAAACTTGAGCAACCCGAGTCTGGATTCCTCGGAGAGTCCTCAG 7029

QY 946 CTGTCCTCCGCTTGTGCGGGGCCCCAGAGTCTGAGGGGACCACTGGCCGTGTGGC 1001  
Db 7028 CTGTCCTCCGCTTGTGCGGGGCCCCAGAGTCTGAGGGGACCACTGGCCGTGTGGC 6973

RESULT 14  
AAV16979  
ID AAV16979 standard; DNA; 4335 BP.  
XX AAV16979;  
AC  
XX  
XX 13-AUG-1998 (first entry)  
DE Human telomerase reverse transcriptase genomic clone.  
XX  
XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;  
KW cell proliferation; cancer; ageing; ribonucleoprotein; ss.  
XX  
XX Homo sapiens.  
XX OS  
XX GB2317891-A.  
XX  
XX 08-APR-1998.  
XX  
XX 01-OCT-1997; 97GB-00020890.  
XX  
XX 01-OCT-1996; 96US-00724643.  
XX 18-APR-1997; 97US-00844419.  
XX 25-APR-1997; 97US-00846017.  
XX 06-MAY-1997; 97US-00851843.  
XX 09-MAY-1997; 97US-00854050.  
XX 14-AUG-1997; 97US-00911312.  
XX 14-AUG-1997; 97US-00912951.  
XX 14-AUG-1997; 97US-00915503.  
XX  
XX (GERO-) GERON CORP.  
XX (UYTE-) UNIV TECHNOLOGY CORP.  
XX  
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;  
PI Andrews WH;  
XX WPI; 1998-171633/16.  
XX  
XX Pure and recombinant human Telomerase Reverse Transcriptase and its  
PT variants - are useful in the diagnosis, prognosis and treatment of cell  
PT proliferation conditions especially cancer and ageing.  
XX  
XX Example 3; Fig 21; 387pp; English.  
XX  
XX The present sequence represents a human telomerase reverse transcriptase  
CC (hTERT) genomic clone from the present invention. The present invention  
CC also describes the following methods: (A) determining whether a test  
CC compound is a modulator of hTERT, by detecting the change in hTERT  
CC recombinant protein or polynucleotide, on administration of the compound;  
CC (B) preparation of recombinant telomerase by contacting a protein  
CC preparation of hTERT with a telomerase RNA component; (C) detection of the  
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample  
CC and detecting the complex formed or in the case of RNA detection,  
CC amplifying the product and correlating the presence of complex or  
CC amplification product with presence of hTERT in the sample; and (D)  
CC increasing the proliferation of a vertebrate cell by increasing hTERT  
CC expression; and (E) the use of an agent that causes an increase in cell  
CC vertebrate cell proliferation to create a medicament that inhibits  
CC ageing. A protein preparation of hTERT and the polynucleotide encoding  
CC hTERT can be used in the manufacture of medicaments for inhibiting the  
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used  
CC to treat conditions that are associated with high telomerase activity. A  
CC protein preparation of hTERT can also be used in the new methods  
XX  
XX Sequence 4335 BP; 698 A; 1416 C; 1360 G; 861 T; 0 U; 0 Other;  
SQ

Query Match 93.0%; Score 930.8; DB 2; Length 4335;  
Best Local Similarity 99.1%; Pred. No. 5.5e-270;

	Matches	999;	Conservative	0;	Mismatches	2;	Indels	7;	Gaps	6;
QY	1	GGCTGGGATTTACAGGACCCCGCCACCATGCCCAGCTAAATTTTGTATTTTGTAGTAGAGA	60							
Db	438	GGCTGGGATTTACAGGACCCCGCCACCATGCCCAGCTAAATTTTGTATTTTGTAGTAGAGA	497							
QY	61	CGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA	120							
Db	498	CGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA	557							
QY	121	TGATCCACCTGCTCTGCTCTTAAAGTGTGGGATTTACAGGCTGGGACCACTGATGCCA	180							
Db	558	TGATCCACCTGCTCTGCTCTTAAAGTGTGGGATTTACAGGCTGGGACCACTGATGCCA	617							
QY	181	GCTCAGAAATTTACTCTCTTTAGAAACATCTGGGCTCTGAGGTAGGAAGCTCACCCACTCA	240							
Db	618	GCTCAGAAATTTACTCTCTTTAGAAACATCTGGGCTCTGAGGTAGGAAGCTCACCCACTCA	677							
QY	241	AGTGTGTGTGTTTTAAAGCAATGATAGAAATTTTTTTTATTTGTTGTAGAACACTCTTGA	300							
Db	678	AGTGTGTGTGTTTTAAAGCAATGATAGAAATTTTTTTTATTTGTTGTAGAACACTCTTGA	737							
QY	301	TGTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAGACACACTAACTGCAACC	360							
Db	738	TGTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAGACACACTAACTGCAACC	797							
QY	361	ATAATACCTGGGGTGTCTTCTGGGTATCAGCATCTTCAATGAAATCGCGGAGGGTTC	420							
Db	798	ATAATACCTGGGGTGTCTTCTGGGTATCAGCATCTTCAATGAAATCGCGGAGGGTTC	857							
QY	421	TGCGCATGCATGGTGTAAATTAATCTCCAGCATTAATCTTCTGCTTCCATTTCTCTTC	480							
Db	858	TGCGCATGCATGGTGTAAATTAATCTCCAGCATTAATCTTCTGCTTCCATTTCTCTTC	917							
QY	481	CTCTTTTAAATTTGTTGTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGTAGCTACA	540							
Db	918	CTCTTTTAAATTTGTTGTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGTAGCTACA	977							
QY	541	ACTTAACTTTTGTGGAAACAAATTTTCCAAACCCCTTTGCTTCCCTAGTGGCAGACAA	600							
Db	978	ACTTAACTTTTGTGGAAACAAATTTTCCAAACCCCTTTGCTTCCCTAGTGGCAGACAA	1037							
QY	601	TTCAAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCG	660							
Db	1038	TTCAAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCG	1097							
QY	661	ACCGTAAATCC-TAAGTATTTTCAAGACAGGCTAACTCCAGCGAGGCTGACAGCCAG	719							
Db	1098	ACCGTAAATCC-TAAGTATTTTCAAGACAGGCTAACTCCAGCGAGGCTGACAGCCAG	1157							
QY	720	GGAGGGTGGAGGCTGTTCAAAATGCTA--GCTCCATAAATAAAGC-AAATTTCTCCGGC	776							
Db	1158	GGAGGGTGGAGGCTGTTCAAAATGCTAAGCTTCAATAAATAAGCAAAATTTCTCCGGC	1217							
QY	777	AGTTTCT- GAAAGTAGGAAAGGTT-ACAATTTAAGTTGCGTTTGTAGCATTTCAAGTGT	834							
Db	1218	AGTTTCTGGAAGTAGGAAAGGTTAAACATTTAAGTTGCGTTTGTAGCATTTCAAGTGT	1277							
QY	835	TGCGGACCTCAGCT-ACAGCATCCCTGCAAGGCTTCGGGAGACCCAGAAAGTTTCTCGCC	893							
Db	1278	TGCGGACCTCAGCTAACAGCATCCCTGCAAGGCTTCGGGAGACCCAGAAAGTTTCTCGCC	1337							
QY	894	CTTAGATCCAACTTTAGCAACCCGGAGTCTGGATTCCTCGGAGTCTCTCAGCTGTCTG	953							
Db	1338	CTTAGATCCAACTTTAGCAACCCGGAGTCTGGATTCCTCGGAGTCTCTCAGCTGTCTG	1397							
QY	954	CGGTGTGCGGGGCCCCCAGGTCTGGAGGGGACCAAGTGGCCGTGTGGC 1001								
Db	1398	CGGTGTGCGGGGCCCCCAGGTCTGGAGGGGACCAAGTGGCCGTGTGGC 1445								

ID AAD27972 standard; DNA; 35871 BP.  
AC AAD27972;  
XX  
DT 16-JUL-2002 (first entry)  
XX  
DE Recombinant adenovirus vector KD3-TERT.  
XX  
KW Recombinant adenovirus vector; adenovirus death protein; ADP; telomerase;  
KW human; telomerase reverse transcriptase promoter; TERT; neoplastic cell;  
KW cancer; KD3-TERT; E1A region; mutant; ds.  
XX  
OS Mastadenovirus.  
OS Homo sapiens.  
OS Synthetic.  
OS Chimeric.  
XX  
XX US2002028785-A1.  
XX  
XX 07-MAR-2002.  
XX  
XX 19-SEP-2001; 2001US-00956335.  
XX  
XX 12-JUL-1999; 99US-00351778.  
PR 20-SEP-2000; 2000US-0233872P.  
XX  
XX (UYSL-) UNIV SAINT LOUIS.  
PA  
XX  
XX Wold WSM, Toth K, Tollefson AE, Kuppuswamy M;  
XX WPI; 2002-328910/36.  
XX  
XX Novel recombinant adenovirus vector useful for destroying neoplastic  
PT cells, comprises a human telomerase reverse transcriptase promoter and at  
PT least one inactivation mutation in the E3 region.  
XX  
XX Claim 5; Page 28-44; 64pp; English.  
XX  
CC The invention relates to a recombinant adenovirus vector which  
CC overexpresses an adenovirus death protein (ADP) and which is replication-  
CC restricted to cells expressing telomerase, comprises a human telomerase  
CC reverse transcriptase promoter (hTERT) and at least one inactivating  
CC mutation in the E3 region. The vector of the invention is useful in vitro  
CC for promoting death of a cell expressing telomerase, and for promoting  
CC death of neoplastic cells in a patient. The adenovirus vector is an  
CC efficient and effective anticancer agent that could specifically target  
CC neoplastic cells, while replicating poorly or not at all in normal  
CC tissue, and efficiently spreading to neighbouring neoplastic cells,  
CC thereby maximising its cancer-killing ability. The presence of human  
CC telomerase reverse transcriptase promoter allows restriction of  
CC replication of the adenovirus to cells expressing telomerase without the  
CC need for complementation to achieve replication competence in these  
CC cells. The present sequence is adenovirus vector KD3-TERT which comprises  
CC an ADP gene, a hTERT promoter, and a mutation in the E1A region  
XX  
XX Sequence 35871 BP; 8238 A; 10114 C; 10001 G; 7518 T; 0 U; 0 Other;  
SQ  
Query Match 67.7%; Score 677.8; DB 6; Length 35871;  
Best Local Similarity 99.7%; Pred. No. 4.7e-193;  
Matches 679; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 321 AAGCATCATCAGCTTTTCAAAGACACACTAACTGACCCCATATACTACCTGCTCTTCT 380  
DB 35713 AAGTAATCATCAGCTTTTCAAAGACACACTAACTGACCCCATATACTACCTGCTCTTCT 35654  
QY 381 GGGTATCAGCATCTTCATTAAGCGGGAGGGTTTCTCGCCATGCACATGGTGTTA 440  
DB 35653 GGGTATCAGCATCTTCATTAAGCGGGAGGGTTTCTCGCCATGCACATGGTGTTA 35594  
QY 441 ATTACTCCAGCATATCTTCGTGCTCCATTTCTTCTCTCCCTCTTTAAATTTGTTT 500  
DB 35593 ATTACTCCAGCATATCTTCGTGCTCCATTTCTTCTCTCCCTCTTTAAATTTGTTT 35534

QY 501 TCTATGTGGCTTCTCTGCAGAGAACACAGTGTAAGCTACAACTTAACCTTTTGTGGACA 560  
DB 35533 TCTATGTGGCTTCTCTGCAGAGAACACAGTGTAAGCTACAACTTAACCTTTTGTGGACA 35474  
QY 561 AATTTTCCAAACCGCCCTTTGCCCCTAGTGGCAGAGACAATTCACAAACACAGCCCTTTTA 620  
DB 35473 AATTTTCCAAACCGCCCTTTGCCCCTAGTGGCAGAGACAATTCACAAACACAGCCCTTTTA 35414  
QY 621 AAAAGGCTTAGGATCACTAAGGGGATTTCTAGAGAGCGACCCGTTAATCTTAAGTATTT 680  
DB 35413 AAAAGGCTTAGGATCACTAAGGGGATTTCTAGAGAGCGACCCGTTAATCTTAAGTATTT 35354  
QY 681 ACAAGCAGAGCTAACTCCAGCGAGCGTGCACAGCCCGAGGGTCCGAGGCCCTGTCA 740  
DB 35353 ACAAGCAGAGCTAACTCCAGCGAGCGTGCACAGCCCGAGGGTCCGAGGCCCTGTCA 35294  
QY 741 AATGCTAGCTCCATAAATAAAGCAATTTCTCCGGCAGTTTCTGAAAGTAGGAAAGTTA 800  
DB 35293 AATGCTAGCTCCATAAATAAAGCAATTTCTCCGGCAGTTTCTGAAAGTAGGAAAGTTA 35234  
QY 801 CATTTAAGGTTGCGTTTGTAGCATTTTCAGTGTTCGCGACCTCAGCTACAGCATCCCTG 860  
DB 35233 CATTTAAGGTTGCGTTTGTAGCATTTTCAGTGTTCGCGACCTCAGCTACAGCATCCCTG 35174  
QY 861 CAAGGCTCCGGAGACCCAGAAAGTTTCTCGCCCTTAGATCCAAACTTGAGCAACCCGGA 920  
DB 35173 CAAGGCTCCGGAGACCCAGAAAGTTTCTCGCCCTTAGATCCAAACTTGAGCAACCCGGA 35114  
QY 921 GTCTGATTCTCGGAAAGTCTCAGCTGTCTCGGGTTGTGCGGGGCCCCAGGCTCTGGA 980  
DB 35113 GTCTGATTCTCGGAAAGTCTCAGCTGTCTCGGGTTGTGCGGGGCCCCAGGCTCTGGA 35054  
QY 981 GGGGACCAAGTGGCCGTGTGTC 1001  
DB 35053 GGGGACCAAGTGGCCGTGTGTC 35033

Search completed: January 10, 2006, 11:12:06  
Job time : 693.667 secs

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OM nucleic - nucleic search, using sw model

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10562.520 Million cell updates/sec

Title: US-09-615-039-1\_COPY\_11500\_12500

Perfect score: 1001

Sequence: 1 ggctggattacaggccccc.....gggaccagtgccgtgtggc 1001

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_in.\*

3: gb\_env.\*

4: gb\_em.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pr.\*

9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vi.\*

14: gb\_htg.\*

15: gb\_pl.\*

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1001	100.0	4321	6	AR390473 Sequence
2	1001	100.0	15332	8	AF121948 Homo sapi
3	1001	100.0	15418	6	AR342806 Sequence
4	1001	100.0	15418	6	AR490112 Sequence
5	1001	100.0	15418	6	AR576878 Sequence
6	1001	100.0	15418	6	AX453025 Sequence
7	1001	100.0	15418	6	AX498409 Sequence
8	1001	100.0	15418	6	AX504952 Sequence
9	1001	100.0	92564	8	AY007685 Homo sapi
c 10	1001	100.0	161252	14	AC114955 Homo sapi
c 11	999.4	99.8	202305	8	AC114291 Homo sapi
c 12	989.8	98.9	170646	14	AC123545 Homo sapi
c 13	989.8	98.8	4356	6	AF097365 Homo sapi
14	972.8	97.2	5126	6	AX003120 Sequence
15	972.8	97.2	5491	8	AB016767 Homo sapi
16	972.8	97.2	11276	6	AX003122 Sequence
17	972.8	97.2	26414	8	AF128893 Homo sapi
18	972.8	97.2	51552	6	AR366023 Sequence

c 19	956	95.5	2501	6	CQ972301	Sequence
c 20	954.4	95.3	7928	6	CS105926	Sequence
c 21	930.8	93.0	4335	6	E36796	Human telom
c 22	930.8	93.0	4335	6	AR393087	Sequence
c 23	930.8	93.0	4335	6	AX810041	Sequence
c 24	930.8	93.0	4335	6	BD011047	Human tel
c 25	916.6	91.6	12213	8	AF114847	AF114847 Homo sapi
c 26	815.4	81.5	170946	14	AC117933	AC117933 Papio anu
c 27	815.4	81.5	183506	14	AC122155	AC122155 Papio anu
c 28	677.8	67.7	35871	6	AR403724	Sequence
c 29	677.8	67.7	35978	6	AR403723	Sequence
c 30	676	67.5	1677	6	AR403725	Sequence
c 31	676	67.5	2043	8	AF098956	AF098956 Homo sapi
c 32	643.2	64.3	4356	6	AX356510	Sequence
c 33	636	63.5	4356	6	AX356509	Sequence
c 34	623.8	62.3	2501	6	CQ972392	Sequence
c 35	623.4	62.3	2501	6	CQ972391	Sequence
c 36	622.2	62.2	7928	6	CS105948	Sequence
c 37	620.2	62.0	7928	6	CS105947	Sequence
c 38	588.6	58.8	2501	6	CQ972486	Sequence
c 39	588.6	58.8	7928	6	CS105970	Sequence
c 40	588.2	58.8	2501	6	CQ972485	Sequence
c 41	586.6	58.6	7928	6	CS105969	Sequence
c 42	497	49.7	497	6	AR576897	Sequence
c 43	320.2	32.0	1404	8	AB018788	Homo sapi
c 44	229.8	23.0	4200	6	AR243331	Sequence
c 45	205.6	20.5	1404	6	AX280011	Sequence

ALIGNMENTS

RESULT 1	AR390473	AR390473	4321 bp	DNA	linear	PAT 18-DEC-2003
LOCUS	Sequence 6 from patent US 6610839.					
DEFINITION	AR390473					
ACCESSION	AR390473.1	GI:40112397				
VERSION						
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 4321)					
AUTHORS	Morin, G.B. and Andrews, W.H.					
TITLE	Promoter for telomerase reverse transcriptase					
JOURNAL	Patent: US 6610839-A 6 26-AUG-2003;					
FEATURES	Location/Qualifiers					
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Best Local Similarity	100.0%	Pred. No.	4.8e-280;				
Matches	1001;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	GGCTGGGATTACAGCACC	CGCCGCCACCATGCTGCTCGAACTTCTGACCTCAGA	60			
Db	438	GGCTGGGATTACAGCACC	CGCCGCCACCATGCTGCTCGAACTTCTGACCTCAGA	497			
Qy	61	CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA	120				
Db	498	CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA	557				
Qy	121	TGATCCACCTGCCTCTGCTCTAAAGTCTGGGATTCAGGTGAGGCACCATGCCCA	180				
Db	558	TGATCCACCTGCCTCTGCTCTAAAGTCTGGGATTCAGGTGAGGCACCATGCCCA	617				
Qy	181	GCTCAGATTACTCTGTTTGAACATCTGGGCTGAGGTAGGAGCTCACCCACTCA	240				
Db	618	GCTCAGATTACTCTGTTTGAACATCTGGGCTGAGGTAGGAGCTCACCCACTCA	677				

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Qy |||||  
301 TGTGTTTACACTGTGATGACCTAAGACATCATCAGCTTTTCAAGACACACTAACTGCACCC 360  
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361 ATAATACCTGGGGTGTCTTCTGGGTATCAGGATCTTCATTTGAATCGGGAGGGTTTCC 420  
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Qy |||||  
421 TCGCCATGCATGCTGTATTAATTAATCTCCAGCATATCTTCTGCTTCCATTCTTCTTTC 480  
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Qy |||||  
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Qy |||||  
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Db |||||  
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Qy |||||  
961 GCGGGGCCCCAGGTCTGGAGGGGACCAAGTGGCGTGTGGC 1001  
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1398 GCGGGGCCCCAGGTCTGGAGGGGACCAAGTGGCGTGTGGC 1438

RESULT 2  
AF121948 15332 bp DNA linear PRI 11-APR-1999  
LOCUS Homo sapiens telomerase reverse transcriptase (TERT) gene, partial cds.  
DEFINITION  
ACCESSION AF121948  
VERSION AF121948.1 GI:4580662  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 15332)  
AUTHORS Greenberg,R.A., O'Hagan,R.C., Deng,H., Xiao,Q., Hann,S.R., Adams,R.R., Lichtsteiner,S., Chin,L., Morin,G.B. and DePinho,R.A.  
TITLE Telomerase reverse transcriptase gene is a direct target of c-Myc but is not functionally equivalent in cellular transformation  
JOURNAL Oncogene 18 (5), 1219-1226 (1999)  
PUBMED 10022128

REFERENCE 2 (bases 1 to 15332)  
AUTHORS Morin,G.B., Carlos,R. and Adams,R.R.  
TITLE Direct Submission  
JOURNAL Submitted (21-JAN-1999) Geron Corporation, 230 Constitution Drive, Menlo Park, CA 94025, USA  
FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
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CDS join(13502..13720,13825..>15178)  
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Query Match 100.0%; Score 1001; DB 8; Length 15332;  
Best Local Similarity 100.0%; Pred. No. 5.5e-280;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 11517 CGGGGTGGGGTGGGGTTCACCATGTCGCCAGGCTGCTCGAACTTCTGACCTCAGA 11576  
Qy 121 TGATCCACCTGCTGCTCTCTTAAAGTGTCTGGGATTACAGGTGTGAGCCACCATGCCA 180  
Db 11577 TGATCCACCTGCTGCTCTCTTAAAGTGTCTGGGATTACAGGTGTGAGCCACCATGCCA 11636  
Qy 181 GCTCAGAAATTTACTGTTTGTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCACTCA 240  
Db 11637 GCTCAGAAATTTACTGTTTGTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCACTCA 11696  
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Db 11697 AGTGTGTGGTGTATTAAGCAATGATAGAAATTTTATTTATTTGTGTAGAACACTCTTGA 11756  
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Db 11817 ATAATACCTGGGGTGTCTTCTGGGTATCAGGATCTTCATTTGAATCGGGAGGGTTTCC 11876  
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Db |||||



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Db 12117 ACCGTAATCTTAAGTATTTTAAAGAGAGAGGCTTAAAGGATCACTAAGGGGATTTCTAGAGAGCG 12176
Qy 721 GAGGTCGAGGCTGTTTAAAGGCTTAAAGGATCACTAAGGGGATTTCTAGAGAGCG 780
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RESULT 3
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LOCUS AR342806 15418 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6576464.
ACCESSION AR342806
VERSION AR342806.1 GI:33738009
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15418)
AUTHORS Gold, J.D. and Lebkowski, J.S.
TITLE Methods for providing differentiated stem cells
JOURNAL Patent: US 6576464-A 1 10-JUN-2003;
Geron Corporation; Menlo Park, CA
FEATURES
Location/Qualifiers
source 1..15418
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Query Match 100.0%; Score 1001; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.5e-280;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 11500 GGCTGGGATTACAGGACCGCCGACCATGCCCCAGCTAATTTTGTATTTTGTAGTAGAGA 11559
Qy 61 CGGGGGTGGGGTGGGGTTCACATGTTGGCCAGGCTGCTCGAATCTTCGACCTCAGA 120
Db 11560 CGGGGGTGGGGTGGGGTTCACATGTTGGCCAGGCTGCTCGAATCTTCGACCTCAGA 11619
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Db 11620 TGATCCACCTGCCTCTGCTCTCTAAAGTGTGGGATTAAGGTCGAGTCGAGCCACCAATGCCA 11679
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Db 11680 GCTCAGAAATTTACTCTGTTTAAAGATCATCTGGGCTCTGAGGTAGGAAGCTCACCCTCA 11739
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Qy 721 GAGGTCGAGGCTGTTTAAAGGCTTAAAGGATCACTAAGGGGATTTCTAGAGAGCG 780
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Qy 841 CCTCAGCTACAGCATCTCTGCAAGGCTTAAAGGCTTAAAGGATCACTAAGGGGATTTCTAGAGAGCG 900
Db 12340 CCTCAGCTACAGCATCTCTGCAAGGCTTAAAGGCTTAAAGGATTTCTAGAGAGCG 12399
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AR490112
LOCUS AR490112 15418 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 1 from patent US 6713055.
ACCESSION AR490112
VERSION AR490112.1 GI:47257268
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15418)
AUTHORS Schiff, J.M.
TITLE Glycosyltransferase vectors for treating cancer
JOURNAL Patent: US 6713055-A 1 30-MAR-2004;
Geron Corporation; Menlo Park, CA
FEATURES
Location/Qualifiers
source 1..15418
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Query Match      100.0%; Score 1001; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.5e-280;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGTGGGATTACAGGACCCGCGCACCATGCGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 60
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Qy 541 ACTTAACCTTTGTGGAAACAAATTTTCCAAACCGCCCTTTTGGCCCTAGTGGGAGAGCAA 600
Db 12040 ACTTAACCTTTGTGGAAACAAATTTTCCAAACCGCCCTTTTGGCCCTAGTGGGAGAGCAA 12099

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Qy 961 GCCGGGGCCCCAGTCTGGAGGGGACCAAGTGGCCGTGTGGC 1001
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Db 12460 GCCGGGGCCCCAGTCTGGAGGGGACCAAGTGGCCGTGTGGC 12500

RESULT 5

AR576878

LOCUS

DEFINITION

AR576878

AR576878

AR576878

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ORIGIN

Query Match 100.0%; Score 1001; DB 6; Length 15418;  
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VERSION  
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LOCUS Homo sapiens telomerase catalytic subunit (TERT) and sodium
DEFINITION channel-like protein genes, complete cds.
ACCESSION AY007685
VERSION AY007685.2 GI:15991796
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SOURCE Homo sapiens
ORGANISM Homo sapiens
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Leem,S.H., Londono-Vallejo,J.A., Kim,J.H., Bui,H., Tubacher,E.,
Solomon,G., Park,J.E., Horikawa,I., Kouprina,N., Barrett,J.C. and
Larionov,V.
The human telomerase gene: complete genomic sequence and analysis
of tandem repeat polymorphisms in intronic regions
Oncogene 21 (5), 769-777 (2002)
JOURNAL PUBMED 11850805
REFERENCE 2 (bases 1 to 92564)
AUTHORS Londono-Vallejo,J.A.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Centre d'Etudes du Polymorphisme Humain, 27
rue Juliette Dodu, Paris 75010, France
AUTHORS Londono-Vallejo,J.A.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2001) Centre d'Etudes du Polymorphisme Humain, 27
rue Juliette Dodu, Paris 75010, France
REMARK Sequence update by submitter
COMMENT On Oct 10, 2001 this sequence version replaced gi:12642956.
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LOCUS AC114291

DEFINITION Homo sapiens chromosome 5 clone CTD-3080P12, complete sequence.

ACCESSION AC114291

VERSION AC114291.2 GI:28973811

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 202305)

DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 202305)

DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 202305)

DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (15-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On Mar 15, 2003 this sequence version replaced gi:19224940..

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.sbgc.stanford.edu

Quality: Phrap Quality >=40 99.9% of Sequence;

Estimated Total Number of Errors is 0.2.

NOTE: Transposon sequencing failed to verify number of repeat copies 173000-175780. Unsure number of repeat copies 173000-175780. BAC and subclones unstable 76080. Force join at 76080.

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Qy 721 GAGGTCGAGGCTGTTCAATAGCTAGCTCCATAAATAAGCAATTTCTCCGGCAGTT 780

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Qy 841 CCTCAGCTACAGCATCTCCCTCAGAGGCTTCGGAGACCCAGAGTTTCTCCGCCCTTAGAT 900

Db 180201 CCTCAGCTACAGCATCTCCCTCAGAGGCTTCGGAGACCCAGAGTTTCTCCGCCCTTAGAT 180142

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 AC123545  
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 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Pan.  
 REFERENCE 1 (bases 1 to 170646)  
 AUTHORS Antonellis, A., Ayele, K., Becketrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K.,  
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 Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K.,  
 Vost, J.L., Wetherby, K.D., Young, A. and Green, E.D.  
 NISC Comparative Sequencing Initiative  
 Unpublished  
 2 (bases 1 to 170646)  
 Green, E.D.  
 Direct Submission  
 TITLE Submitted (30-MAY-2002) NIH Intramural Sequencing Center, 8717  
 JOURNAL Government Circle, Gaithersburg, MD 20877, USA  
 REFERENCE 3 (bases 1 to 170646)  
 Green, E.D.  
 Direct Submission  
 TITLE Submitted (25-JUL-2003) NIH Intramural Sequencing Center, 8717  
 JOURNAL Government Circle, Gaithersburg, MD 20877, USA  
 COMMENT On Jul 25, 2003 this sequence version replaced gi:24414279.  
 ----- Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: <http://www.nisc.nih.gov>  
 Contact: [nisc.zoo@hghri.nih.gov](mailto:nisc.zoo@hghri.nih.gov)  
 ----- Project Information  
 Center project name: cmz  
 Center clone name: 165N09

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.  
 ----- Summary Statistics  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 16710 bases at least Q40  
 Consensus quality: 168559 bases at least Q30  
 Consensus quality: 169363 bases at least Q20  
 Insert size: 152000; agarose-fp  
 Insert size: 169746; sum-of-contigs

Quality coverage: 11.31x in Q20 bases; agarose-fp  
 Quality coverage: 10.13x in Q20 bases; sum-of-contigs  
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 \* NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 \* 1 6384: contig of 6384 bp in length  
 \* 6385: gap of unknown length  
 \* 37411: contig of 30927 bp in length  
 \* 37412: gap of unknown length  
 \* 37512: contig of 8840 bp in length  
 \* 46451: gap of unknown length  
 \* 46452: contig of 5365 bp in length  
 \* 51817: gap of unknown length  
 \* 51917: contig of 16060 bp in length  
 \* 67976: gap of unknown length  
 \* 67977: contig of 46604 bp in length  
 \* 114681: gap of unknown length  
 \* 114682: contig of 6871 bp in length  
 \* 121651: gap of unknown length  
 \* 121751: contig of 4180 bp in length  
 \* 125931: gap of unknown length  
 \* 125932: contig of 2325 bp in length  
 \* 126032: gap of unknown length  
 \* 128357: contig of 42190 bp in length.  
 \* 128457: Location/Qualifiers  
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DEFINITION	Homo sapiens telomerase reverse transcriptase (TERT) gene, promoter and partial cds.		
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VERSION	AF097365.1	GI:4210970	
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ORGANISM	Homo sapiens		
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REFERENCE	1 (bases 1 to 4356)		
AUTHORS	Cong Y.S., Wen,J. and Bacchetti,S.		
TITLE	The human telomerase catalytic subunit hTERT: organization of the gene and characterization of the promoter		
JOURNAL	Hum. Mol. Genet. 8 (1), 137-142 (1999)		
PUBMED	9887342		
REFERENCE	2 (bases 1 to 4356)		
AUTHORS	Cong Y.S., Wen,J. and Bacchetti,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-OCT-1998) Pathology, McMaster University, 1200 Main St. W., Hamilton, ON L8N 3Z5, Canada		
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DEFINITION Sequence 1 from Patent WO9933998.  
ACCESSION AX003120  
VERSION AX003120.1 GI:9926982  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
Wick, M. and Hagen, G.  
AUTHORS Regulatory dna sequences of the human catalytic telomerase sub-unit  
TITLE gene, diagnostic and therapeutic use thereof  
JOURNAL Patent: WO 9933998-A 1 08-JUL-1999;  
WICK MARESA (DE); BAYER AG (DE)

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RESULT 15
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DEFINITION Homo sapiens gene for telomerase transcriptase, partial cds.
ACCESSION AB016767
VERSION AB016767.1 GI:4239869
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Takakura,M., Kyo,S., Kanaya,T., Hirano,H., Takeda,J., Yutsudo,M.
and Inoue,M.
TITLE Cloning of human telomerase catalytic subunit (hTERT) gene promoter
and identification of proximal core promoter sequences essential
for transcriptional activation in immortalized and cancer cells
Cancer Res. 59 (3), 551-557 (1999)
JOURNAL 9973199
PUBMED 2 (bases 1 to 5491)
REFERENCE Takakura,M., Kyo,S., Kanaya,T., Takeda,J. and Inoue,M.
AUTHORS Direct Submission
TITLE Submitted (04-AUG-1998) Masahiro Takakura, Kanazawa University,
JOURNAL School of Medicine, Department of Obstetrics and Gynecology; 13-1,
Takaramachi, Kanazawa, Ishikawa 920-0934, Japan
(E-mail:takakura@med.kanazawa-u.ac.jp, Tel:81-76-265-2425,
Fax:81-76-234-4266)
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/protein_id="BAA74724.1"
/db_xref="GI:4239870"
translation="MPRAPRCRAVRLLRSHRYEVLPLATFVRRLGPGQWRLLVQRGDP
AAFRALVAQCLVCPWDARPPAPSPRQVSCLELVARVLQRLCERGANVLAFGFA
LLDARGGPEAFETTSVRSYLPNTVTDALRGAGWGLLRVGDVLLVHLLARCALPV
LVAPSCAYQVCGPLVOLGAATQARPAPHASGPRRLGCEAWNHSVREAGVPLGLPA
PGARRGGSASRLPLPKPRRGAAPERPFPVQGSWAHPGRTGFSRDFGVCVSPA
RPABEATLSEALSGNTHSPSVGRQHAGPPSTSRPPRPWDPFCPPVVAETKHFLYS
SGDKQLRPLFSLSSRLPILTGARLIVETIFLGSFGCQGLPAGCPACSPATGKCPG
FWSCLGTFRAGTPGCSRRPTARCLRSPPQSPVSPGRSPRALWRPRRTQTPTVWCS
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3634. 3737
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3738. 5088
/gene="hTERT"

intron
exon
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intron
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5089. >5491
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/number=2

ORIGIN
Query Match 97.2%; Score 972.8; DB 8; Length 5491;
Best Local Similarity 99.5%; Pred. No. 8.1e-272;
Matches 997; Conservative 0; Mismatches 2; Indels 3; Gaps 2;

Qy 1 GGCTGGGATTACAGGCACCGCCACCATGCCCCAGCTAAATTTTGTGATTATTTTATGTTAGTAGAGA 60
Db 1371 GGCTGGGATTACAGGCACCGCCACCATGCCCCAGCTAAATTTTGTGATTATTTTATGTTAGTAGAGA 1430
Qy 61 CGGGGGTGGGGTGGGGTTCACCATCTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 120
Db 1431 CGGGGGT--GGGGTGGGGTTCACCATCTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 1488
Qy 121 TGATCCACCTGCCCTCTGCCCTCTTAAAGTGTCTGGGATTACAGGTGTGAGCCACCACCATGCCCA 180
Db 1489 TGATCCACCTGCCCTCTGCCCTCTTAAAGTGTCTGGGATTACAGGTGTGAGCCACCACCATGCCCA 1548
Qy 181 GCTCAGAAATTTACTCTGTTTAGAAAACATCTGGGTCTGAGTAGGAAAGCTCACCCCACTCA 240
Db 1549 GCTCAGAAATTTACTCTGTTTAGAAAACATCTGGGTCTGAGTAGGAAAGCTCACCCCACTCA 1608
Qy 241 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTATTTGTTGTAGAACACTCTTGA 300
Db 1609 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTATTTGTTGTAGAACACTCTTGA 1668
Qy 301 TGTTTTTACACTGTGATGACTTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
Db 1669 TGTTTTTACACTGTGATGACTTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 1728
Qy 361 ATAATACTGGGGTGTCTTCTGGGTATCAGCATCTTCATTGAATCCGGGAGGCGTTTCC 420
Db 1729 ATAATACTGGGGTGTCTTCTGGGTATCAGCAATCTTCATTGAATCCGGGAGGCGTTTCC 1788
Qy 421 TCGCCATGACATGGTGTAAATTTACTCCAGCATAATCTTCTGCTTCATTTCTCTCTCTTC 480
Db 1789 TCGCCATGACATGGTGTAAATTTACTCCAGCATAATCTTCTGCTTCATTTCTCTCTCTTC 1848
Qy 481 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGACAGAAACAGTGTAAAGTACTACA 540
Db 1849 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGACAGAAACAGTGTAAAGTACTACA 1908
Qy 541 ACTTAACTTTTGTGGAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGGAGAGACAA 600
Db 1909 ACTTAACTTTTGTGGAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGGAGAGACAA 1968
Qy 601 TTCAAAACACAGCCCTTTTAAAGGCTTAGGATCACTAAGGGGATTTCTAGAGAGCG 660
Db 1969 TTCAAAACACAGCCCTTTTAAAGGCTTAGGATCACTAAGGGGATTTCTAGAGAGCG 2028
Qy 661 ACCGTAATCTTAAGTATTATTAAGACAGAGGCTTAACTCCAGCGAGCGGTAGGATTTCTAGAGAGCG 720
Db 2029 ACCGTAATCTTAAGTATTATTAAGACAGAGGCTTAACTCCAGCGAGCGGTAGGATTTCTAGAGAGCG 2088
Qy 721 GAGGGTGCAGGCGCTGTTCAAATGCTAGCTCCATAAATAAGCAATTTCTCCGGCAGTT 780
Db 2089 GAGGGTGCAGGCGCTGTTCAAATGCTAGCTCCATAAATAAGCAATTTCTCCGGCAGTT 2148
Qy 781 TCTGAAAGTAGGAAAGGTTACATTTAAGTGTGGTTTGTAGCATTTCACTGTTTCCCGA 840
Db 2149 TCTGAAAGTAGGAAAGGTTACATTTAAGTGTGGTTTGTAGCATTTCACTGTTTCCCGA 2208
Qy 841 CCTCAGCTACAGCATCCCTCGAAGGCTCGGGAGACCCAGAAGTTTCTCG-CCCTTTAGA 899
Db 2209 CCTCAGCTACAGCATCCCTCGAAGGCTCGGGAGACCCAGAAGTTTCTCGCCCTTAGA 2268
Qy 900 TCCAAACTTGAGCAACCCGAGTCTCGAATTCCTGGGAAGTCTCAGCTGCTGCGGTTG 959
Db 2269 TCCAAACTTGAGCAACCCGAGTCTCGAATTCCTGGGAAGTCTCAGCTGCTGCGGTTG 2328
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**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 05:49:50 ; Search time 4711 Seconds  
(without alignments)  
9941.386 Million cell updates/sec

Title: US-09-615-039-1\_COPY\_9500\_10500  
Perfect score: 1001  
Sequence: 1 aaagaccagcattggcac.....ggattatttcaaaacaagg 1001

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues  
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	59	5.9	752	10 AG030352	AG030352 Pan trogl
C 2	56.2	5.6	410	2 BF873304	BF873304 CM0-ET012
C 3	55.4	5.5	925	10 CNS0091P	AL053013 Drosophil
C 4	52	5.2	541	6 CF790496	CF790496 875629 MA
C 5	50.8	5.1	660	10 C8820739	C8820739 tigr-gss-
C 6	50.2	5.0	976	5 BQ707318	BQ707318 AGENCOURT
C 7	50	5.0	825	6 CD653180	CD653180 AGENCOURT
C 8	49.2	4.9	525	9 AQ405885	AQ405885 HS_5043 B
C 9	48.4	4.8	439	9 AQ112190	AQ112190 CIT-HSP-2
C 10	47.8	4.8	313	2 BG952375	BG952375 PM4-CT056
C 11	47.6	4.8	780	9 CC539630	CC539630 CH240_419
C 12	46.2	4.6	1101	10 CNS017SY	AL08460 Drosophil
C 13	45.8	4.6	481	9 B46953	B46953 HS-1066-A2-
C 14	45.6	4.6	584	5 BW968443	BW968443 BW968443
C 15	45.6	4.6	791	10 CL003114	CL003114 gbsl VM5
C 16	45.4	4.5	576	10 CF740534	CF740534 tigr-gss-
C 17	45.4	4.5	625	7 CO616290	CO616290 DG9-155J5
C 18	45.4	4.5	868	5 BX422116	BX422116 BX422116
C 19	44.8	4.5	651	10 CL323295	CL323295 RPCI144_45
C 20	44.8	4.5	1116	5 BX404837	BX404837 BX404837
C 21	44.8	4.5	1120	5 BX404704	BX404704 BX404704
C 22	44.6	4.5	688	5 BX674306	BX674306 BX674306

23	44.6	4.5	808	11	CR869506	CR869506 Sus scrofa
24	44	4.4	470	8	H60898	H60898 Yr46h12.81
25	44	4.4	538	9	AQ535541	AQ535541 RPCI-11-3
26	43.6	4.4	1101	10	CNS00397	AL063912 Drosophil
27	43.4	4.3	836	2	BG844208	BG844208 1024005E0
28	43.4	4.3	948	10	CNS001CB	AL074499 Drosophil
29	43.2	4.3	573	10	CE754698	CE754698 tigr-gss-
30	43.2	4.3	744	10	CNS0172K	AL108698 Drosophil
31	43.2	4.3	835	9	AZ205689	AZ205689 SP_0101 B
32	43.2	4.3	912	10	CNS006N3	AL065775 Drosophil
33	43	4.3	589	10	AG190202	AG190202 Pan trogl
34	43	4.3	784	9	BZ605806	BZ605806 WHAW54TF
35	43	4.3	964	10	CNS003WG	AL065254 Drosophil
36	43	4.3	1309	10	CL080957	CL080957 CH216-160
37	42.8	4.3	420	8	R56134	R56134 YG94f07.81
38	42.8	4.3	762	10	CW914345	CW914345 RPCI42_15
39	42.8	4.3	765	1	AW448342	AW448342 BRY_588 B
40	42.8	4.3	766	5	BQ609726	BQ609726 BRY_588 w
41	42.8	4.3	793	11	CR897177	CR897177 Sus scrofa
42	42.8	4.3	814	11	CR897197	CR897197 Sus scrofa
43	42.6	4.3	386	9	CE152959	CE152959 tigr-gss-
44	42.6	4.3	510	9	AQ677422	AQ677422 HS_5529 A
45	42.6	4.3	613	10	AG043036	AG043036 Pan trogl

ALIGNMENTS

RESULT 1  
AG030352/c  
LOCUS Pan troglodytes DNA, clone: PTB-002L10.R, genomic survey sequence.  
DEFINITION AG030352 752 bp DNA linear GSS 01-NOV-2001  
ACCESSION AG030352  
VERSION AG030352.1 GI:16557225  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Pan.  
REFERENCE 1  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Totoki, Y., Watanabe, H. and Sakaki, Y.  
TITLE BAC end sequences of Library PTB  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 752)  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Totoki, Y., Watanabe, H. and Sakaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: chimbe@gsr.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the Rad process and may have higher chance of  
clone tracking errors.  
PRIMERS  
Sequencing: M13Rev  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI  
Location/Qualifiers  
1. 752  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-002L10.R"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"

FEATURES  
source

ORIGIN

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/dev_stage="Adult"
/clone_lib="ET0121"
/notes="Organ: lung tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match      5.6%; Score 56.2; DB 2; Length 410;
Best Local Similarity 60.8%; Pred. No. 0.0006;
Matches 161; Conservative 0; Mismatches 98; Indels 6; Gaps 4;

QY 582 GCCCCAGGCGCTTTGCGAGGTGTGATCTCCGTGAGGACCCCTGAGGTCTGG-GATCCTTCGG 640
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 379 GCAAGAGGACTTTGCGAGGCGCATTTAGGTTAAAGGCTCTGAGATGAGGTGATCATTTCTG 320
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 641 GACTACTGCGAGCCCGCAAAAGTAATC-CAGGGGTTCTGGAAAGAGCGCGGAGAGGGGT 699
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 319 GATTATCTAAGGGGGGCCCAATGTCTATCACAAGGTTCTTGGAATGTGTCGCAAGAGGGT 260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 700 CAG---AGGGGGCAGCCTCAGGACGATGAGGAGCAGTCACTCTGAGGCTGAAAAGGAGG 756
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 259 CAGATTAGAGGAGATGGTGAAGGGTAGCAGTGAATTTGAGAGTGAAGATGGA 200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 757 GAGGGCTCGAGCCCGAGGCGCTGCAAGCGCTCCAGAAAGCTGGAAGAGCGGGGAAG-GGA 815
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 199 TGGGGCCATGATCAAGGAATGTGGGCACCCCTGAAAGCTGGAAGTCAAGGAAGCAGA 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 816 CCTCCACGAGGCTCGCAGCAGAA 840
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 139 CCCTCCCTGGAGCCTCTCTGAAGAA 115
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
CNS0091P/c      925 bp      DNA      linear      GSS 03-JUN-1999
LOCUS           Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION      BAC19D16 of RPCI-98 library from Drosophila melanogaster (fruit
KEYWORDS         fly), genomic survey sequence.
SOURCE           AL053013
ORGANISM         Drosophila melanogaster (fruit fly)
AUTHORS          GSS.
COMMENT          Drosophila melanogaster
                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                  Ephydroidea; Drosophilidae; Drosophila.
REFERENCE        1 (bases 1 to 925)
AUTHORS          Genoscope.
TITLE            Direct Submission
JOURNAL          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
COMMENT          BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
                  - Web : www.genoscope.cns.fr)
                  Determination of this BAC-end sequence was carried out as part of a
                  collaboration with the Berkeley Drosophila Genome Project (BDGP).
                  The BDGP is constructing a physical map of the Drosophila
                  melanogaster genome using these BACs. For further information
                  please see http://www.fruitfly.org The BDGP Drosophila
                  melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                  Aaron Mammeter in Pieter de Jong's laboratory in the Department of
                  Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                  NY. The library is named RPCI-98 and was constructed by partial
                  EcoRI digestion of Drosophila DNA provided by the BDGP from the
                  isogenic strain y2; cn bw sp, the same strain used for the BDGP's
                  P1 and EST libraries. A more detailed description of the library
                  and how to order individual BAC clones, the entire library, or
                  filters for hybridization from the BACPAC Resource Center can be
                  found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES         Location/Qualifiers
source           1..925

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QY 578 CCGGGCCCGAGGGCCTTTTGAGGTGTGATCTCCGTGAGGACCCCTGAGGTCTGGGATCCTT 637
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 243 CACAGCAAACTGACCTTGACATGCGATTAAAGTTAAGGATCTTGAGTTGGGGTTAAAT 302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 638 CGGACTACTCTGACGGCCCGAAAGTAATCAAGGGGTTCTGGGAAGAGCGGGCGAGG 697
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 303 TGGATCATCTGAGAGGCCCTTTTATAAATACAAGAGTCCCTTATATAAAGGGAGACAGAAG 362
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 698 GTCAAGGGGGGAGCCCTCAGGACGATGGAGCAGTCAGTCTGAGGCTGAAAGGGAGGG 757
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 363 CTCAGAATCAGGGGGAGATTGAAGATGCTGCCCTGTGTGGTGTGGAAGAGAGA - 421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 758 AGGCGCTCGAGCCGAGCCCTGCAAGCGCTCCAGAGCTCGAAAAGCGGGAGGGAGCC 817
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 --GGCTTGGCCNAGAAATGCGAGCAGCTCTTGAGCTGGAGAGACGAGAACACATT 479
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 818 CTCAC-GGAGCTCTGACGAGGAGGACCGCTG 850
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 480 TTCTCTAGAGCTCCAGGAGGACACAGCTCTG 513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
BQ707318/c
LOCUS
DEFINITION
AGENCOURT 8353488 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279801
5', mRNA sequence.
ACCESSION
BQ707318
VERSION
BQ707318.1 GI:21846217
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 976)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2469 row: p column: 10
High quality sequence stop: 580.
FEATURES
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:6279801"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_113"
            /notes="Organ: spleen; Vector: pOTB7; Site:1: XhoI; Site:2:
            EcoRI; cDNA made by oligo-dT priming. Directionally cloned
            into EcoRI/XhoI sites using the following 5' adaptor:
            GGACACGAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
            NIH_MGC Library."
ORIGIN
Query Match 5.0%; Score 50.2; DB 5; Length 976;
Best Local Similarity 59.7%; Pred. No. 0.032;
Matches 105; Conservative 0; Mismatched 73; Indels 1; Gaps 1;
QY 681 AAGAGCGGGGAGGAGGCTCAGAGGGGGGAGCGCTCAGGACGATGGAGGAGTCAGTCTG 740
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 538 AAGAGGGAGGTAGGAGGTGAGTGCAGGGGTGAGAGGAGAGCCAGAGAGCGCTATGCTG 479
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 741 AGCTGAAAAGGGAGGGAGGGCTTCAGCCAGCGCTGCAAGCGCTCCAGAACTCGAA 800
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 478 CTGGCTGGGAGATGGACGAGGCCACCAAGCCCAAGGAATGCAGGGGGCTCTCTGGAAGCTGAA 419
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 801 AAAGCGGGGAAG-GGACCCCTCCACGAGCGCTGCAGCAGGAGGACGACGCGCTGGCCCTTAG 858
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 AAGCAGAGGAACGATTTCTCCAGACCCCGAGGACACGCGCTGCTGGACCTTG 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
CD653180
LOCUS
DEFINITION
AGENCOURT_14551916 NIA Human H1 Embryonic Stem Cell cDNA Library
(long) Homo sapiens cDNA clone IMAGE:30425811 5', mRNA sequence.
CD653180
CD653180.1 GI:31891231
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 825)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-remail.nih.gov
Tissue Procurement: Irene Ginis and Mahendra Rao, NTA
cDNA Library Preparation: Yulan Piao and Minoru KO
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM510 row: k column: 04
High quality sequence stop: 686.
FEATURES
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:30425811"
            /tissue_type="Embryonic Stem cells"
            /cell_line="WA01"
            /lab_host="DH10B (T1 phage-resistant)"
            /clone_lib="NIA Human H1 Embryonic Stem Cell cDNA Library
            (Long)"
            /notes="Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI;
            This is a long-transcript enriched cDNA library (Genome
            Res. 11: 1553-1558 (2001). [PMID: 11544199]) from WA01
            cell line. Undifferentiated human ES cell line WA01/H1
            was obtained from WiCell Research Institute, Inc.,
            Madison, WI, cultured according to their instructions, on
            MEF feeders. They formed round colonies with defined edges
            and were positive for alkaline phosphatase, SSEA-4, OCT3,
            OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45. They are
            negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLT3, SSEA-1,
            TUBB3, NES, GFAP, and BOMBS. When confluent (18-10 days
            after plating), the ES cells from 4 x 6cm dishes were
            treated with 1 mg/ml collagenase, type IV
            (Invitrogen/GIBCO) for 5-10 min and gently scraped off
            with 5 ml pipette. RNA was purified with TRIzol Reagent
            from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558
            (2001). [PMID:11544199]] Double-stranded cDNAs were
            synthesized with an oligo(dT) primer [Invitrogen:
            5'-pGACTAGTTCTAGATCGGAGCGCGCCCTTTTTTTTTTTT-3'] from

```

3.4g of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to L-one-linker Li-Sal4, purified by phenol/chloroform extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The average insert size is about 3.6kb."

## ORIGIN

Query Match 5.0%; Score 50; DB 6; Length 825;  
 Best Local Similarity 69.4%; Pred. No. 0.035;  
 Matches 68; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 743 GCTGAAAGGAGGAGGAGGCTCGAGCCAGGCTCGAAGCGCTCCAGAGCTGGAAAA 802  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 440 GCTGCTTGAAGAGGAGGCGCCATGAGCCAGGCGGATGCGAGCACCTCCAGAGCTGGAATT 499  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 803 AGCGGGAGGAGGACCTCCAGCGAGCTCGACAGGAA 840  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 500 GCCAGGAAGGAGATCTCCCTCGAGCTTCCAGAAAGAA 537  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

## RESULT 8

AQ405885/c  
 LOCUS AQ405885 525 bp DNA linear GSS 13-MAR-1999  
 DEFINITION HS 5043 B2 P07 T7 RPCI-11 Human Male BAC Library Homo sapiens genomic\_clone Plates=619 Col=14 Row=L, genomic survey sequence.  
 ACCESSION AQ405885  
 VERSION AQ405885.1 GI:4415873  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 525)  
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
 TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
 PUBMED 10449764  
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu  
 Plate: 619 Row: L Column: 14  
 Seq primer: 77  
 Class: BAC ends  
 High quality sequence stop: 525.  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="Plate=619 Col=14 Row=L"  
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FEATURES  
source

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/note="Vector: pBACE3.6; Site\_1: EcoRI; Site\_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

## ORIGIN

Query Match 4.9%; Score 49.2; DB 9; Length 525;  
 Best Local Similarity 59.4%; Pred. No. 0.052;  
 Matches 120; Conservative 0; Mismatches 78; Indels 4; Gaps 2;

Qy 611 GTGAGGACCTCTGGAGTCTCTGGGATCTCTCGGACTTACTTCGAGGCCCGGAAAAGTAATCCAG 670  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 317 GTGATTGGATTGAGGATCTTCAGATGAGGAGATTATCTGGGTGGCCCTAAAGTAATCACA 258  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 671 GGGTTCTGGAGAGGCGGCGAGGAGGTCTCAGAGGGGGGCGAGCCCTCAGGACGATGGAGGC 730  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 257 GGGGTCTTATGAGCAGGAGGCGAGGGGTCTAGATCTCAGACAGACTGGAAGATGC---C 201  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 731 AGTCAGTCTGAGGCTGAAAAAGGAGGAGGCGCTTCGAGCCCGGAGCCCTGCAAGC-GCCTCC 789  
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 Db 200 ACCTGTTGCTTTGAAGTGGAGAGGGGCCATGAGCCAAGGCATGCAGGCAGCTTCC 141  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 790 AGAAGCTGGAAGAAAGCGGGGAA 811  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 140 ACAAGCTGGAAGAAAGGAA 119  
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## RESULT 9

AQ112190  
 LOCUS AQ112190 439 bp DNA linear GSS 29-AUG-1998  
 DEFINITION CIT-HSP-2373021.TR CIT-HSP Homo sapiens genomic clone 2373021, genomic survey sequence.  
 ACCESSION AQ112190  
 VERSION AQ112190.1 GI:3484350  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 439)  
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.  
 TITLE Use of a random human BAC End Sequence Database for Sequence-Ready Map Building  
 JOURNAL Unpublished (1998)  
 COMMENT Other GSSs: CIT-HSP-2373021.TF  
 Contact: Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: mdadams@tigr.org  
 Clones are available from Research Genetics (info@resgen.com). BAC end search page:  
 http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html.  
 Seq primer: M13 Reverse  
 Class: BAC ends.  
 Location/Qualifiers  
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## ORIGIN

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Best Local Similarity 55.2%; Pred. No. 0.082;
Matches 179; Conservative 0; Mismatches 136; Indels 9; Gaps 4;

Qy 532 AGAGATCCCAAGCTCTGATTCCTCCCAAACTGTGGACAGAACCCCGCCGCCAGGGC 591
    |||||
Db 79 AAAGATGCTCCATGTAATTT-CCAGAAATCTGTGAATATTACTTACCTGTGTAAGGGA 137
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Qy 592 CTTTGAGGTGTGATCTCCGTGAGACCTGAGTCTGG-GATCCTTCGGGACTACCTGC 650
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Db 138 TTTTGCAGATCGCACTAGTTAAGGCTCTTCGCAATGTGGAGACGCTCTCGATGATTCAG 197
    |||||

Qy 651 AGGCCCGAAAGTAATCCAGGGTTCCTGGGAAGAGCGCGGAGGAGGTTCAGAGGGGGC 710
    |||||
Db 198 GTGGGCCCTACGTAATCCCTAGGCTCTTATCAGGGGAGGAAGAGATCAGTCGGAAGA 257
    |||||

Qy 711 AGCCTCAGGACGATGAGGAGTCTGAGTCTGAGGCTGAAAAGGAGGAGGAGGCTTCAGACC 770
    |||||
Db 258 GAGATTAGAGGTGCTATGCTGT-----TGAATTTGAGATGAGGAAGCGGCACAGCC 312
    |||||

Qy 771 CAGGCTGCAAGCGCTTCAGAGCTGGAAGCTGAAAAGCGGGGAGGAGCCCT--CAGCGAGC 828
    |||||
Db 313 AAGGAGTGCAGGTGGCTCCAGAGTAGAAGCAAGGAATGAATTTTCCAGAGAGC 372
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Qy 829 CTCGAGCAGGAAGCACGGCTGGC 852
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Db 373 CTCATGAAGGAATGCAGTTCTGCC 396
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RESULT 10
BG952375/c
LOCUS          313 bp      mRNA      linear      EST 12-JUN-2001
DEFINITION    PM4-CT0562-170101-009-e10 CT0562 Homo sapiens cDNA, mRNA sequence.
ACCESSION    BG952375
VERSION      BG952375.1 GI:14370546
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE     1 (bases 1 to 313)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
              Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
              Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
              10737800
              Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-CT0562-
              170101-009-e10&t3=2001-01-17&t4=1)
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/notes="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORSTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN
Query Match      4.8%; Score 47.8; DB 2; Length 313;
Best Local Similarity 56.8%; Pred. No. 0.11;
Matches 88; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 691 CAGAGAGGTTCAGAGGGGGGAGCCTCAGGACGATGGAGGAGTCAGTCTCAGGCTGAAA 750
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Db 203 CACAAGAGGATGGGGGGGGCTGTATCAGAGCGGTGACGTCAGACGAGGCGAGGC 144
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Qy 751 GCGAGGGAGGGCTTCGAGCCCGAGGCTCGAAGCGCTCCAGAGCTCGAAGAGCGGGGA 810
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Db 143 TGGGGTGATCTCAGGGCTGCACCAAGGGGCGAGCGGCTTCAGACGCTGGAGAGCGGGAA 84
    |||||

Qy 811 AGGAGCCCTCCAGCGAGCCTGTCAGCAGGAGGAC 845
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Db 83 ACGGGGTCTCTGGGAGCCCGCCAGAAAGACCCAC 49
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RESULT 11
CC539630/c
LOCUS          780 bp      DNA      linear      GSS 17-JUN-2003
DEFINITION    CH240_419J4.TABBAC13P2 CHORI-240 Bos taurus genomic clone
              CH240_419J4, genomic survey sequence.
ACCESSION    CC539630
VERSION      CC539630.1 GI:31857914
KEYWORDS      GSS.
SOURCE        Bos taurus (cow)
ORGANISM      Bos taurus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
              Pecora; Bovidae; Bovinae; Bos.
              1 (bases 1 to 780)
REFERENCE     Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
              Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M., Chiu,R.,
              Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
              Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
              Schein,J., Marra,M., de Jong,P., Keele,J.W. and Kappes,S.M.
              Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
              Unpublished (2003)
              Other GSSs: CH240_419J4.T7
              Contact: Rob Holt
              Sequencing
              The British Columbia Cancer Agency Genome Science Centre
              600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6
              Tel: 604-877-6085
              Fax: 604-877-6276
              Email: rholt@bccsc.ca
              Clones are derived from the bovine BAC library CHORI-240
              (http://www.chori.org/bacpac/bovine240.htm). For BAC library
              availability, please contact Pieter de Jong (pdejong@mail.cho.org).
              Clones may be purchased from BACPAC Resources
              (http://www.chori.org/bacpac/ordering/information.htm). This work
              was undertaken as part of the International Bovine BAC Mapping
              Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
              British Columbia Genome Sciences Centre, Canada.
              Plate: 419 row: J column: 4
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

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Searched: 4637633 seqs, 364532575 residues

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Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61.2	6.1	191684	7	US-11-121-086-2
2	55	5.5	33737	6	US-10-276-233A-7
3	55	5.5	175100	7	US-11-121-086-21
4	49.8	5.0	1707	6	US-10-750-185-60686
5	49.8	5.0	1707	6	US-10-750-623-60686
6	45.8	4.6	203467	7	US-11-121-086-50
7	42.8	4.3	96256	6	US-10-775-189-352
8	41.2	4.0	120096	7	US-11-121-086-24
9	40.4	4.0	319608	7	US-11-145-703-1
10	39	3.9	5651	6	US-10-750-185-38240
11	39	3.9	5651	6	US-10-750-623-38240
12	38.8	3.9	191350	6	US-10-857-780-4
13	38.6	3.9	4136	7	US-11-136-527-2296
14	38.4	3.8	126552	7	US-11-121-086-1
15	38	3.8	185393	7	US-11-121-086-101
16	37.6	3.8	75007	6	US-10-995-561-13194
17	37.2	3.7	2055	6	US-10-750-185-46360
18	37.2	3.7	2055	6	US-10-750-623-46360
19	37	3.7	51749	6	US-10-995-561-13245
20	37	3.7	168516	7	US-11-121-086-3
21	36.4	3.6	175673	7	US-11-121-086-55
22	36	3.6	150468	7	US-11-112-908-56
23	36	3.6	193789	7	US-11-112-908-55

c 24	35.6	3.6	20945	6	US-10-995-561-13463	Sequence 13463, A
c 25	35.6	3.6	23082	6	US-10-995-561-13457	Sequence 13457, A
c 26	35.6	3.6	94510	6	US-10-995-561-13332	Sequence 13332, A
c 27	35.4	3.5	792	7	US-11-102-883-35	Sequence 35, Appl
c 28	35.4	3.5	825	7	US-11-102-883-33	Sequence 33, Appl
c 29	35.4	3.5	1608	6	US-10-750-185-37878	Sequence 37878, A
c 30	35.4	3.5	1608	6	US-10-750-623-37878	Sequence 37878, A
c 31	35.4	3.5	4360	7	US-11-109-157A-21	Sequence 21, Appl
c 32	35.2	3.5	40000	6	US-10-995-561-13510	Sequence 13510, A
c 33	35.2	3.5	171486	7	US-11-121-086-105	Sequence 105, App
c 34	35.2	3.5	179777	7	US-11-121-086-106	Sequence 106, App
c 35	35	3.5	79528	6	US-10-276-233A-6	Sequence 6, Appl
c 36	35	3.5	84409	6	US-10-995-561-13494	Sequence 13494, A
c 37	35	3.5	86131	6	US-10-995-561-13298	Sequence 13298, A
c 38	34.8	3.5	137935	6	US-10-995-561-13278	Sequence 13278, A
c 39	34.8	3.5	285300	6	US-10-857-780-6	Sequence 6, Appl
c 40	34.6	3.5	600	7	US-11-136-527-5440	Sequence 5440, Ap
c 41	34.6	3.5	974	7	US-11-136-527-1344	Sequence 1344, Ap
c 42	34.6	3.5	172111	7	US-11-121-086-28	Sequence 28, Appl
c 43	34.4	3.4	200628	7	US-11-121-086-62	Sequence 62, Appl
c 44	34.2	3.4	201	6	US-10-995-561-38077	Sequence 38077, A
c 45	34.2	3.4	201	6	US-10-995-561-54894	Sequence 54894, A

ALIGNMENTS

RESULT 1  
US-11-121-086-2  
; Sequence 2, Application US/11121086  
; Publication No. US20050266459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121.086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 191684  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-11-121-086-2

Query Match	6.1%	Score 61.2;	DB 7;	Length 191684;
Best Local Similarity	52.5%	Pred. No. 8.4e-08;		
Matches 191;	Conservative 0;	Mismatches 158;	Indels 15;	Gaps 2;
Qy	550	ATTCCCCCAACCTGTGGACAGAACCCGCCGCCAGGCGCTTTGAGTGTGATCTC	609	
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Qy	610	CGTCAGACCTGAGTCTGGATCCTTCGGGACTACTGCGAGCCCGGAAAGTAATCCA	669	
Db	113438	AACAAAGACCTCGAGGGTGGTGAACATTTGATATTCGGGAACCCAGTGCCTCAC	113497	
Qy	670	GGGGTTCGGGACAGCGCGGACAGGGTTCAGAGGGGGGCGCTCAGGACGATGGAGG	729	
Db	113498	AGGGTCTTTTAAAGAGGAGGACAGGGGTGAGAGTCAAGAGACTGAAAGGCTGTGC	113557	
Qy	730	CAGTCAGTCTGAGCTGAAAGAGGAGGAGGGCTTCGAGCCAGGCTTCGAAGCGCTCC	789	
Db	113558	-----TGTGGTTCGAGGAGGAGGCGCCCTGAGCCGAGGATGCGAGTGCCTCC	113610	
Qy	790	AGAGCTGGAAAAAGCGGGAGGAGGACCTTCACGAGCCTTCAGCAGC	841	
Db	113611	AGATGCTGGAAAGCGGGCACTGACTCTCCCGAAGCCTTCGGGAGCCCACTGCTGC	113670	
Qy	842	GCACGGCTGGCCCTTAGCCACCAGGGGCCATCGTGGACCTCCGCGCTCCGTCATAGG	901	







OTHER INFORMATION: exon Q1 complement g34872 gene  
FEATURE:  
NAME/KEY: exon  
LOCATION: 229647..229742  
OTHER INFORMATION: exon X complement g34872 gene  
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NAME/KEY: exon  
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OTHER INFORMATION: exon P complement g34872 gene  
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LOCATION: 231272..231412  
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NAME/KEY: exon  
LOCATION: 239719..239807  
OTHER INFORMATION: exon N2 complement g34872 gene  
FEATURE:  
NAME/KEY: exon  
LOCATION: 239719..239853  
OTHER INFORMATION: exon N complement g34872 gene  
FEATURE:  
NAME/KEY: exon  
LOCATION: 240528..240569  
OTHER INFORMATION: exon M1117 complement g34872 gene  
FEATURE:  
NAME/KEY: exon  
LOCATION: 240528..240596  
OTHER INFORMATION: exon M1090 complement g34872 gene  
FEATURE:  
NAME/KEY: exon  
LOCATION: 240528..240617  
OTHER INFORMATION: exon M1069 complement g34872 gene  
FEATURE:  
NAME/KEY: exon  
LOCATION: 240528..240644  
OTHER INFORMATION: exon MS2 complement g34872 gene  
FEATURE:  
NAME/KEY: exon  
LOCATION: 240528..240824  
OTHER INFORMATION: exon M862 complement g34872 gene  
FEATURE:  
NAME/KEY: exon  
LOCATION: 240528..240994  
OTHER INFORMATION: exon M692 complement g34872 gene  
FEATURE:  
NAME/KEY: exon  
LOCATION: 240528..241685  
OTHER INFORMATION: exon M1 complement g34872 gene  
FEATURE:  
NAME/KEY: exon  
LOCATION: 240800..240993  
OTHER INFORMATION: exon MS1 complement g34872 gene  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 241686..243685  
OTHER INFORMATION: 5 regulatory region g34872 gene

FEATURE:  
NAME/KEY: misc feature  
LOCATION: 290652..292652  
OTHER INFORMATION: 3'regulatory region g34665 gene  
Query Match 4.0%; Score 40.4; DB 7; Length 319608;  
Best Local Similarity 60.2%; Pred. No. 0.31;  
Matches 100; Conservative 1; Mismatches 62; Indels 3; Gaps 2;  
Qy 694 GAGGGTCAGAGGGGGGCGAGCCTCAGGACGATGGAGGAGTCAGTCTCAGGCTGAAAGGG 753  
Db 238738 GAGAGGGGGATGCTGGGAAGAAGAGTGTCTCAGAGAAGCAACATTGCTGACTCTAAAGACAG 238797  
Qy 754 AGGGAGGGCCTCGAGGCCAGGCCCTGCAAG-CGCTCCAGAAAGCTGGAAAAGC--GGGGA 810  
Db 238798 AGGCGAGCCACGAGCCAGGCATGCGAGGAGGCTCCAGAAAGCTGGGCGAGCAAGAGAA 238857  
Qy 811 AGGGACCTCCAGGAGCCTGCGAGCAGGAAGGCGAGGCTGGCCCTT 856  
Db 238858 TGGACTCAGCCCTGGAGCCTCCAGAAGGCATGCGAGCCTGCCCATT 238903

## RESULT 10

US-10-750-185-38240  
; Sequence 38240, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; PRIOR FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38240  
; LENGTH: 5651  
; TYPE: DNA  
; ORGANISM: Bovine 19866880256159  
US-10-750-185-38240

Query Match 3.9%; Score 39; DB 6; Length 5651;  
Best Local Similarity 57.1%; Pred. No. 0.12;  
Matches 109; Conservative 0; Mismatches 80; Indels 2; Gaps 2;  
Qy 517 GCAGGATAAGTCTTAGAGATGCCAGTCTGTGATTTCCCAACC-TGTGGACAGAAC 575  
Db 1690 GCAGGACAAAGTCCAGAGATGTCCCTCTCTGATCCCGCCCAAGAGGACGCGGCC 1749  
Qy 576 CGCCCGGCCCGAGGCTTTCAGGTGTGATCTCGTGAGGACCTGAGGTCTGGATCC 635  
Db 1750 CGACAGACAAAGGGGCTTCGGGGTGTGATTAGTGACA-GACCTTGATGGGACATT 1808  
Qy 636 TTGGGAGTACCTCGAGCCCGGAAAGTAATCCAGGGGTCTCGGAAGAGCGGCGCAGGA 695  
Db 1809 GTCCCGATTGTCTGGGTGGCCCGTGCATCACCAGGGTCTGAAACAGCGGGGGGG 1868  
Qy 696 GGGTCAGAGGG 706  
Db 1869 GGCACGGAGGG 1879

## RESULT 11

US-10-750-623-38240  
; Sequence 38240, Application US/10750623  
; Publication No. US20050287531A1



Db 140228 CATAAAGGTGAAACAAAGAGGTTAGAGGGGACACAAAGGAGGGAGGCCACCAGGCCAGGCA 140169  
Qy 776 CTGCAAGCGCTCCAGAGCTTGGAAAAGCGGGAA 811  
Db 140168 TGCAGGTGGCTTCTGGAAAGCTTGGAAAAGCGCAAGGAA 140133

RESULT 13  
US-11-136-527-2296  
; Sequence 2296, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; PRIOR FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2296  
; LENGTH: 4136  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-2296

Query Match 3.9%; Score 38.6; DB 7; Length 4136;  
Best Local Similarity 56.8%; Pred. No. 0.14;  
Matches 71; Conservative 0; Mismatches 54; Indels 0; Gaps 0;  
Qy 676 CTGGGAAGCGCGGCGAGGGTTCAGAGGGGGCGAGCTTCAGGACGATGAGGCGAGTCA 735  
Db 71 CAGGAAGCACGACGCGGGGAGCAGGCAAGGGGGCGAGCGCCCGCGCCAGGTTGCC 130  
Qy 736 GTCTGAGGCTGAAAAGGAGGAGGGCTTCAGAGCCAGGCTGCAAGCGCTCCAGGAAGC 795  
Db 131 GTGAGAGGCTCGCGGGGAGGAGTCAGTCTTACCCAGGCGACCGAGGACCTTCAGACGG 190  
Qy 796 TGGAA 800  
Db 191 TAGCA 195

RESULT 14  
US-11-121-086-1/c  
; Sequence 1, Application US/11121086  
; Publication No. US20050266459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 126552  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-121-086-1

Query Match 3.8%; Score 38.4; DB 7; Length 126552;  
Best Local Similarity 65.7%; Pred. No. 0.82; Mismatches 36; Indels 1; Gaps 1;  
Matches 71; Conservative 0;  
Qy 734 CAGTCTGAGGCTGAAAAGGAGGAGGGCTTCGAGCCAGGCGCTTCAAGCGCTCCAGAA 793

Db 69519 CACTGTGGCTGTGAAGGGGGAGAAAGGGCCCTTAAGATGAGGGATGCGGATCCCTCTTAGAC 69460  
Qy 794 GCTGGAAAAGCGGGGAAGGAGCCCTCCAC-GGAGCCTGCGAGGAA 840  
Db 69459 CTTGGGAAGCGAGGAATGGGTTCTCCCTGGAGCTTCCAGGAGGGA 69412

RESULT 15  
US-11-121-086-101/c  
; Sequence 101, Application US/11121086  
; Publication No. US20050266459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 101  
; LENGTH: 185393  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-121-086-101

Query Match 3.8%; Score 38; DB 7; Length 185393;  
Best Local Similarity 60.8%; Pred. No. 1.3;  
Matches 79; Conservative 0; Mismatches 50; Indels 1; Gaps 1;  
Qy 576 CGCCCGCGCCCGAGGGCTTTGCGAGGTGTGATCTCCGTGAGGACCTCGAGGTCTGGGATCC 635  
Db 116833 CACATGSCAAAAGCGAGTTTGCAGATGTGATTTAATTCAGTATCTTGAGATAGGAGACA 116774  
Qy 636 TTGCGGACTACCTGCGAGGCGCCGAAAAGTAATC-CAGGGGTTCTGGGAAGAGCGCGGCGAGG 694  
Db 116773 TCTTGGATTACCCAGATGGACCCAAAGGGAATCACAGGCTTCTTCAAGAGAGAAACAGA 116714  
Qy 695 AGGTCAGAG 704  
Db 116713 AGAGTCAGAG 116704

Search completed: January 10, 2006, 20:45:46  
Job time : 213.333 secs

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Db 10460 AACCCATGCACTGTGAATCTAGGATTATTTCAAAACAAAGG 10500

RESULT 9

US-10-840-455-1

; Sequence 1, Application US/10840455

; Publication No. US20050032094A1

; GENERAL INFORMATION:

; APPLICANT: Bayer Aktiengesellschaft

; APPLICANT: Hagen, Gustav

; APPLICANT: Wick, Maresa

; APPLICANT: Zubov, Dmitry

; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic

; TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use

; FILE REFERENCE: Lea 32 805C1

; CURRENT APPLICATION NUMBER: US/10/840,455

; CURRENT FILING DATE: 2004-05-06

; PRIOR APPLICATION NUMBER: PCT/EP98/08216

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: US 09/582,246

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: DE19757984.1

; PRIOR FILING DATE: 1997-12-24

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 5126

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-840-455-1

Query Match 98.7%; Score 988.4; DB 8; Length 5126;

Best Local Similarity 99.8%; Pred. No. 6.1e-313;

Matches 1000; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 AAAAGACCCAGCATTTGGCACCCTTGGACATTTGGCCACAGCCCTTGGGAATTCACGTGAC 60

Db 1079 AAAAGACCCAGCATTTGGCACCCTTGGACATTTGGCCACAGCCCTTGGGAATTCACGTGAC 1138

QY 61 TACGCACATCATGTACACATCTCCGTTCACACGACCCCGCTGTGTTTATTTAAATAGC 120

Db 1139 TACGCACATCATGTACACATCTCCGTTCACACGACCCCGCTGTGTTTATTTAAATAGC 1138

QY 121 TACAAGCAGGGAATCTCTTAATGTCTTTACAAATCTGTTTAAACAAACGGGTC 180

Db 1199 TACAAGCAGGGAATCTCTTAATGTCTTTAAATGTCTTTAAACAAATCTGTTTAAACGGGTC 1258

QY 181 CATCGCACGCTGGACAGTCTCTACAGTGAAGAGAACATGCGCTTTTATAAGCTTGCA 240

Db 1259 CATCGCACGCTGGACAGTCTCTACAGTGAAGAGAACATGCGCTTTTATAAGCTTGCA 1318

QY 241 GGCATCTCAAGGGAATTAAGTGTGAGTCAAACTGACCTCCATGGGATAGTACGCAAC 300

Db 1319 GGCATCTCAAGGGAATTAAGTGTGAGTCAAACTGACCTCCATGGGATAGTACGCAAC 1378

QY 301 ATGCTCAAAAGAAAGATTTTCAACCCATGGCAGGGAGTGTTTGGGGGTTAAGGACG 359

Db 1379 ATGCTCAAAAGAAAGATTTTCAACCCATGGCAGGGAGTGTTTGGGGGTTAAGGACG 1438

QY 360 GTGGGGGACAGCTGGGGGCTTACTGACGACACCTTTTAAAGCCAGTTTCTTGTTTC 419

Db 1439 GTGGGGGACAGCTGGGGGCTTACTGACGACACCTTTTAAAGCCAGTTTCTTGTTTC 1498

QY 420 TGATGGTATTGGCTCAGTTATGGGAGACTAACATAGGGAGTGGGGATGGGGGAACCCG 479

Db 1499 TGATGGTATTGGCTCAGTTATGGGAGACTAACATAGGGAGTGGGGATGGGGGAACCCG 1558

QY 480 GAGGCTGTGCCATCTTTGCGATGCCCCGAGTGTCTTGGGAGGATTAATCTCTAGATGTC 539

Db 1559 GAGGCTGTGCCATCTTTGCGATGCCCCGAGTGTCTTGGGAGGATTAATCTCTAGATGTC 1618

QY 540 CCAGCTCTGATTTCCCTCAAACTCTGTGACAGAACCCCGCCCGCCAGGGGCTTTGCGAG 599

RESULT 10

US-10-840-455-3

; Sequence 3, Application US/10840455

; Publication No. US20050032094A1

; GENERAL INFORMATION:

; APPLICANT: Bayer Aktiengesellschaft

; APPLICANT: Hagen, Gustav

; APPLICANT: Wick, Maresa

; APPLICANT: Zubov, Dmitry

; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic

; TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use

; FILE REFERENCE: Lea 32 805C1

; CURRENT APPLICATION NUMBER: US/10/840,455

; CURRENT FILING DATE: 2004-05-06

; PRIOR APPLICATION NUMBER: PCT/EP98/08216

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: US 09/582,246

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: DE19757984.1

; PRIOR FILING DATE: 1997-12-24

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3

; LENGTH: 11276

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-840-455-3

Query Match 98.7%; Score 988.4; DB 8; Length 11276;

Best Local Similarity 99.8%; Pred. No. 8.1e-313;

Matches 1000; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 AAAAGACCCAGCATTTGGCACCCTTGGACATTTGGCCACAGCCCTTGGGAATTCACGTGAC 60

Db 7229 AAAAGACCCAGCATTTGGCACCCTTGGACATTTGGCCACAGCCCTTGGGAATTCACGTGAC 7288

QY 61 TACGCACATCATGTACACATCTCCGTTCACACGACCCCGCTGTGTTTATTTAAATAGC 120

Db 7289 TACGCACATCATGTACACATCTCCGTTCACACGACCCCGCTGTGTTTATTTAAATAGC 7348

QY 121 TACAAGCAGGGAATCTCTGTTAAATGTCTTTAAACAAATCTGTTTAAACAAACGGGTC 180

Db 7349 TACAAGACGGGAAATCCCTGCTAAATATGCTTTTAAACAAATGGTTTAAACAAACGGGTC 7408  
Qy 181 CATCCGACCGTGGACAGTTCTCTACAGTGAAGAGGAACATGCGCTTTTATAAAGCCCTGCA 240  
Db 7409 CATCCGACCGTGGACAGTTCTCTACAGTGAAGAGGAACATGCGCTTTTATAAAGCCCTGCA 7468  
Qy 241 GGCATCTCAAGGGAATTTACGCTGAGTCAGTCAAAATCGCCACCTCCATGGGATACGTACGCAAC 300  
Db 7469 GGCATCTCAAGGGAATTTACGCTGAGTCAGTCAAAATCGCCACCTCCATGGGATACGTACGCAAC 7528  
Qy 301 ATGCTCAAAAAGAAAGAAATTTACCCCATGCGAGGAGTGGTT-GGGGGGTTTAAAGACG 359  
Db 7529 ATGCTCAAAAAGAAAGAAATTTACCCCATGCGAGGAGTGGTTTAAAGGAGGTTTAAAGACG 7588  
Qy 360 GTGGGGACAGCTGGGGCTACTGACGACCTTTTACTAAAGCCAGTTTCTGTGTTTC 419  
Db 7589 GTGGGGCGCAGCTGGGGCTACTGACGACCTTTTACTAAAGCCAGTTTCTGTGTTTC 7648  
Qy 420 TGATGGTATTGGCTCAGTTATGGGAGACTAAACATAGGGAGTGGGATGGGGAAACCCG 479  
Db 7649 TGATGGTATTGGCTCAGTTATGGGAGACTAAACATAGGGAGTGGGATGGGGAAACCCG 7708  
Qy 480 GAGCTGTGCCATCTTTGCCATGCTCCGAGTGTCTGTGGCAGGATTAATGCTCTAGAGATGC 539  
Db 7709 GAGCTGTGCCATCTTTGCCATGCTCCGAGTGTCTGTGGCAGGATTAATGCTCTAGAGATGC 7768  
Qy 540 CCAGTCTGATTTCCCGAAACCTGTGGAGACAGAACCCCGCGCCGCGCCAGGCGCTTTGCAG 599  
Db 7769 CCAGTCTGATTTCCCGAAACCTGTGGAGACAGAACCCCGCGCCGCGCCAGGCGCTTTGCAG 7828  
Qy 600 GTGTGATCTCCGTGAGGACCTTCCGAGTCTGGGATCTTCCGGACTACTCTGAGGCGCCGAA 659  
Db 7829 GTGTGATCTCCGTGAGGACCTTCCGAGTCTGGGATCTTCCGGACTACTCTGAGGCGCCGAA 7888  
Qy 660 AAGTAATCCAGGGGTTCTGGGAGAGAGCGGCGAGGAGTCCAGCGAGCCCTGAGCCCTGCG 719  
Db 7889 AAGTAATCCAGGGGTTCTGGGAGAGAGCGGCGAGGAGTCCAGCGAGCCCTGAGCCCTGCG 7948  
Qy 720 ACCATGGAGGACGTCAAGTCTGAGCTGAGTCAAAAGAGGAGGAGGCTCCAGCCAGCCCTGC 779  
Db 7949 ACCATGGAGGACGTCAAGTCTGAGCTGAGTCAAAAGAGGAGGAGGCTCCAGCCAGCCCTGC 8008  
Qy 780 AAGCGCTCCAGAGCTGGGAAAGAGCGGGGAGGAGCCCTCCAGCGAGCCCTGACAGCAGGA 839  
Db 8009 AAGCGCTCCAGAGCTGGGAAAGAGCGGGGAGGAGCCCTCCAGCGAGCCCTGACAGCAGGA 8068  
Qy 840 AGGCAGGCTGGCCCTTTAGCCCAACAGGCGCCATCGTGGACCTCCGCGCTCCGTTGCCATA 899  
Db 8069 AGGCAGGCTGGCCCTTTAGCCCAACAGGCGCCATCGTGGACCTCCGCGCTCCGTTGCCATA 8128  
Qy 900 GGAGGGCACTCGCGCTGCCCTTTAGCATGAGTGTGTGGGATTTGCAAGCAACAGG 959  
Db 8129 GGAGGGCACTCGCGCTGCCCTTTAGCATGAGTGTGTGGGATTTGCAAGCAACAGG 8188  
Qy 960 AAACCCATGCACTGTGAATCTAGGATTTTCAAAACAAAGG 1001  
Db 8189 AAACCCATGCACTGTGAATCTAGGATTTTCAAAACAAAGG 8230

RESULT 11  
US-10-840-455-43  
; Sequence 43, Application US/10840455  
; Publication No. US20050032094A1  
; GENERAL INFORMATION:  
; APPLICANT: Bayer Aktiengesellschaft  
; APPLICANT: Hagen, Gustav  
; APPLICANT: Wick, Mareisa  
; APPLICANT: Zubov, Dmitry  
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic  
; FILE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use  
; FILE REFERENCE: Lea 32 805C1  
; CURRENT APPLICATION NUMBER: US/10/840,455  
; CURRENT FILING DATE: 2004-05-06

; PRIOR APPLICATION NUMBER: PCT/EP98/08216  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: US 09/582,246  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: DE19757984.1  
; PRIOR FILING DATE: 1997-12-24  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 43  
; LENGTH: 26414  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-840-455-43

Query Match 98.7%; Score 988.4; DB 8; Length 26414;  
Best Local Similarity 99.8%; Pred. No. 1.1e-312;  
Matches 1000; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 AAAAGACCCAGCATTTGGCACCCCTGGACATTTGCCCATCCACAGCCCTGGGAATTCACGTTGAC 60  
Db 7229 AAAAGACCCAGCATTTGGCACCCCTGGACATTTGCCCATCCACAGCCCTGGGAATTCACGTTGAC 7288  
Qy 61 TAGCGACATCATGTACACACTCCCGTCCACGACCGACCCCGCTGTTTATTTTAAATAGC 120  
Db 7289 TAGCGACATCATGTACACACTCCCGTCCACGACCGACCCCGCTGTTTATTTTAAATAGC 7348  
Qy 121 TACAAAGCAGGGAATTCCTCTGCTTAAATGTCCTTTTAAACAACTGGTTTAAACAAACGGGTC 180  
Db 7349 TACAAAGCAGGGAATTCCTCTGCTTAAATGTCCTTTTAAACAACTGGTTTAAACAAACGGGTC 7408  
Qy 181 CATCCGACCGTGGACAGTTCTCTACAGTGAAGAGGAACATGCGCTTTTATAAAGCCCTGCA 240  
Db 7409 CATCCGACCGTGGACAGTTCTCTACAGTGAAGAGGAACATGCGCTTTTATAAAGCCCTGCA 7468  
Qy 241 GGCATCTCAAGGGAATTTACGCTGAGTCAAAATCGCCACCTCCATGGGATACGTACGCAAC 300  
Db 7469 GGCATCTCAAGGGAATTTACGCTGAGTCAAAATCGCCACCTCCATGGGATACGTACGCAAC 7528  
Qy 301 ATGCTCAAAAAGAAAGAAATTTACCCCATGCGAGGAGTGGTT-GGGGGGTTTAAAGACG 359  
Db 7529 ATGCTCAAAAAGAAAGAAATTTACCCCATGCGAGGAGTGGTTTAAAGGAGGTTTAAAGACG 7588  
Qy 360 GTGGGGACAGCTGGGGCTACTGACGACCTTTTACTAAAGCCAGTTTCTGTGTTTC 419  
Db 7589 GTGGGGCGCAGCTGGGGCTACTGACGACCTTTTACTAAAGCCAGTTTCTGTGTTTC 7648  
Qy 420 TGATGGTATTGGCTCAGTTATGGGAGACTAAACATAGGGAGTGGGATGGGGAAACCCG 479  
Db 7649 TGATGGTATTGGCTCAGTTATGGGAGACTAAACATAGGGAGTGGGATGGGGAAACCCG 7708  
Qy 480 GAGCTGTGCCATCTTTGCCATGCTCCGAGTGTCTGTGGCAGGATTAATGCTCTAGAGATGC 539  
Db 7709 GAGCTGTGCCATCTTTGCCATGCTCCGAGTGTCTGTGGCAGGATTAATGCTCTAGAGATGC 7768  
Qy 540 CCAGTCTGATTTCCCGAAACCTGTGGAGACAGAACCCCGCGCCGCGCCAGGCGCTTTGCAG 599  
Db 7769 CCAGTCTGATTTCCCGAAACCTGTGGAGACAGAACCCCGCGCCGCGCCAGGCGCTTTGCAG 7828  
Qy 600 GTGTGATCTCCGTGAGGACCTTCCGAGTCTGGGATCTTCCGGACTACTCTGAGGCGCCGAA 659  
Db 7829 GTGTGATCTCCGTGAGGACCTTCCGAGTCTGGGATCTTCCGGACTACTCTGAGGCGCCGAA 7888  
Qy 660 AAGTAATCCAGGGGTTCTGGGAGAGAGCGGCGAGGAGTCCAGCGAGCCCTGAGCCCTGCG 719  
Db 7889 AAGTAATCCAGGGGTTCTGGGAGAGAGCGGCGAGGAGTCCAGCGAGCCCTGAGCCCTGCG 7948  
Qy 720 ACCATGGAGGACGTCAAGTCTGAGCTGAGTCAAAAGAGGAGGAGGCTCCAGCCAGCCCTGC 779  
Db 7949 ACCATGGAGGACGTCAAGTCTGAGCTGAGTCAAAAGAGGAGGAGGCTCCAGCCAGCCCTGC 8008  
Qy 780 AAGCGCTCCAGAGCTGGGAAAGAGCGGGGAGGAGCCCTCCAGCGAGCCCTGACAGCAGGA 839  
Db 8009 AAGCGCTCCAGAGCTGGGAAAGAGCGGGGAGGAGCCCTCCAGCGAGCCCTGACAGCAGGA 8068  
Qy 840 AGGCAGGCTGGCCCTTTAGCCCAACAGGCGCCATCGTGGACCTCCGCGCTCCGTTGCCATA 899  
Db 8069 AGGCAGGCTGGCCCTTTAGCCCAACAGGCGCCATCGTGGACCTCCGCGCTCCGTTGCCATA 8128  
Qy 900 GGAGGGCACTCGCGCTGCCCTTTAGCATGAGTGTGTGGGATTTGCAAGCAACAGG 959  
Db 8129 GGAGGGCACTCGCGCTGCCCTTTAGCATGAGTGTGTGGGATTTGCAAGCAACAGG 8188  
Qy 960 AAACCCATGCACTGTGAATCTAGGATTTTCAAAACAAAGG 1001  
Db 8189 AAACCCATGCACTGTGAATCTAGGATTTTCAAAACAAAGG 8230

Qy	840	AGGCA CGGCTGGGCCCTTAGCCCA CCA GGGGCCATCTGTGACCTCCGGCCCTCCGTCGCATA	899
Db	8069	AGGCACGGCTGGGCCCTTAGCCCA CCA GGGGCCATCTGTGACCTCCGTCGCATA	8128
Qy	900	GGAGGGCACTCGGCTCGCCCTTCTAGCATGAAGTGTGTGGGGATTTCAGAAAGCAACAGG	959
Db	8129	GGAGGGCACTCGGCTCGCCCTTCTAGCATGAAGTGTGTGGGGATTTCAGAAAGCAACAGG	8188
Qy	960	AAACCCATGCACGTGTGAATCTAGGATTTATTTCAAAACAAAGG	1001
Db	8189	AAACCCATGCACGTGTGAATCTAGGATTTATTTCAAAACAAAGG	8230

## RESULT 12

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Db	7349	TACAAACACGAGGAAATCCCTGCTAAATATGCTTTTAAACAACTGGTTTAAACAAACGCGGTC	7408
Qy	181	CATCCGCACCGTGGACAGTTCCTCACAGTGAAGAGGAACATGCGCGTTTATAAAGCCCTGCA	240
Db	7409	CATCCGCACCGTGGACAGTTCCTCACAGTGAAGAGGAACATGCGCGTTTATAAAGCCCTGCA	7468
Qy	241	GGCATCTCAAGGGAAATACGCTGAGTCAAAAATGCCCCACCTCCATGTGGATACGTACGCAAC	300
Db	7469	GGCATCTCAAGGGAAATACGCTGAGTCAAAAATGCCCCACCTCCATGTGGATACGTACGCAAC	7528
Qy	301	ATGCTCAAAAAGAAAGAAATTCACCCCATGCGAGGGAGTGCTT- GGGGGGTTAAGAACG	359
Db	7529	ATGCTCAAAAAGAAAGAAATTCACCCCATGCGAGGGAGTGCTT- GGGGGGTTAAGAACG	7588
Qy	360	GTGGGGCAGCAGCTGTGGGGCTACTGCACGCACCTTTTACTAAAGCCAGTTTCTCTGCTTC	419
Db	7589	GTGGGGCAGCAGCTGTGGGGCTACTGCACGCACCTTTTACTAAAGCCAGTTTCTCTGCTTC	7648
Qy	420	TGATGTTATTTGGCTCAGTTATGGGAGACTAAACCATAGGGAGTGGGATGGGGAAACCGG	479
Db	7649	TGATGTTATTTGGCTCAGTTATGGGAGACTAAACCATAGGGAGTGGGATGGGGAAACCGG	7708
Qy	480	GAGGCTGTGCATCTTTGGCCATGCCCGAGTGTCTCTGGGCGAGTAATATGCTCTAGAGATGC	539
Db	7709	GAGGCTGTGCATCTTTGGCCATGCCCGAGTGTCTCTGGGCGAGTAATATGCTCTAGAGATGC	7768
Qy	540	CCACGTCTCTGATTCCTCCCAAAACCTGTGACAGAACCCGCCGCCGCCAGCGCCCTTTTCAG	599
Db	7769	CCACGTCTCTGATTCCTCCCAAAACCTGTGACAGAACCCGCCGCCGCCAGCGCCCTTTTCAG	7828
Qy	600	GTGTGATCTCCGTGAGGACCTGAGGTCTGGATCTTCGGGACTACCTGCAGGCCCGGAA	659
Db	7829	GTGTGATCTCCGTGAGGACCTGAGGTCTGGATCTTCGGGACTACCTGCAGGCCCGGAA	7888
Qy	660	AAGTAATCCAGGGGTTCTGGGAGAGCGGGCAGGAGGTTCAGAGGGGGCAGCCTCAGG	719
Db	7889	AAGTAATCCAGGGGTTCTGGGAGAGCGGGCAGGAGGTTCAGAGGGGGCAGCCTCAGG	7948
Qy	720	ACGATGAGGCAGTCAGTCTGAGGCTGAAAGGAGGAGGGGCTCCAGGCCCAGGGCCTGC	779
Db	7949	ACGATGAGGCAGTCAGTCTGAGGCTGAAAGGAGGAGGAGGCTCCAGGCCCAGGGCCTGC	8008
Qy	780	AAGCGCTCCAGAAAGCTGTGAAAAAGCGGGGAAAGGACCTTCCACGAGCCTGCAGCAGGA	839
Db	8009	AAGCGCTCCAGAAAGCTGTGAAAAAGCGGGGAAAGGACCTTCCACGAGCCTGCAGCAGGA	8068
Qy	840	AGCAGCGCTGGCCCTTAGCCACAGGGGCCATCTGTGACCTCCGCGCTCCGTGGCCATA	899
Db	8069	AGCAGCGCTGGCCCTTAGCCACAGGGGCCATCTGTGACCTCCGCGCTCCGTGGCCATA	8128
Qy	900	GGAGGGCACTCGGCTGCCCTTCTAGCATGAAGTGTGTGGGGATTTTCAGAAAGCAACAGG	959
Db	8129	GGAGGGCACTCGGCTGCCCTTCTAGCATGAAGTGTGTGGGGATTTTCAGAAAGCAACAGG	8188
Qy	960	AAACCCATGCACTGTGTAATCTAGGATTAATTTCAAAACAAAGG	1001
Db	8189	AAACCCATGCACTGTGTAATCTAGGATTAATTTCAAAACAAAGG	8230

## RESULT 13

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; US-10-456-830-1
; Sequence 1, Application US/10456830
; Publication NO. US20040248246A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Horikawa, Izumi
; APPLICANT: Barrett, J. Carl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DIFFERENTIAL EXPRESSION
; FILE REFERENCE: 4239-63008
; CURRENT APPLICATION NUMBER: US/10/456,830

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494	QY	TTTTGCCATCCCGAGTGTCTCTGGGCGAGGATTAATGCTCTAGAGATGCCCAAGTCTCCTGATTC	553
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554	QY	CCCCAAACCTGTGTGCACAGAACCCCGCCCGCCCGCCAGGGCCTTTGCAGGTGTGATCTCCGTG	613
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600	QY	TTCTGGGAAAGCGCGCAGGAGGTCTCAGAGGGGGCAGCCTCAGGACGATGGAGGACGT	733
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RESULT 14  
US-10-027-632-134480  
; Sequence 134480, Application US/10027632  
; Publication No. US20020190371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 134480  
; LENGTH: 683  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-134480

Query Match 62.5%; Score 625.6; DB 5; Length 683;  
Best Local Similarity 99.8%; Pred. No. 3.4e-194;  
Matches 625; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	376	GGG	GCTACTG	CACGCA	CTTTT	CTAAAG	CCAGTTT	CTGGTT	CTGAT	TGGTAT	TGGCTCA	435		
DB	1	GGG	GCTACTG	CACGCA	CTTTT	CTAAAG	CCAGTTT	CTGGTT	CTGAT	TGGTAT	TGGCTCA	60		
QY	436	GTT	ATGGG	AGACTA	ACCAT	TGGG	GAGTGGG	GAA	CCCG	GAGGCTG	GCATCTT	495		
DB	61	GTT	ATGGG	AGACTA	ACCAT	TGGG	GAGTGGG	GAA	CCCG	GAGGCTG	GCATCTT	120		
QY	496	TGC	CATGCC	CAGTGT	CTCTG	GGCAGG	ATAAT	TGCT	CTAG	AGATGCC	CACTCTGAT	555		
DB	121	TGC	CATGCC	CAGTGT	CTCTG	GGCAGG	ATAAT	TGCT	CTAG	AGATGCC	CACTCTGAT	180		
QY	556	CCA	AACTGT	GGA	CAGAA	CCCG	CCGG	CCCA	GGG	CTTTG	CAGTGTGAT	615		
DB	181	CCA	AACTGT	GGA	CAGAA	CCCG	CCGG	CCCA	GGG	CTTTG	CAGTGTGAT	240		
QY	616	GAC	CTGAG	GTTCTG	GGATC	CTT	CGG	ACTA	CTTG	CAGG	CCCGAA	AGTAATCCAGGGGTT	675	
DB	241	GAC	CTGAG	GTTCTG	GGATC	CTT	CGG	ACTA	CTTG	CAGG	CCCGAA	AGTAATCCAGGGGTT	300	
QY	676	CTG	GGAGAGG	CGG	CAGAG	GGGT	CAG	AGGG	GGG	CAG	CTC	AGGACGATG	735	
DB	301	CTG	GGAGAGG	CGG	CAGAG	GGGT	CAG	AGGG	GGG	CAG	CTC	AGGACGATG	360	
QY	736	GTC	TGAGG	CTG	AAAGG	GAGG	AGGG	CCCT	TC	GAG	CC	CAGG	CCCTC	795
DB	361	GTC	TGAGG	CTG	AAAGG	GAGG	AGGG	CCCT	TC	GAG	CC	CAGG	CCCTC	420
QY	796	TGG	AAAAAG	CGGG	GAGG	GA	CCCT	CCA	GGA	GCCTG	CG	CAGG	AAAG	855
DB	421	TGG	AAAAAG	CGGG	GAGG	GA	CCCT	CCA	GGA	GCCTG	CG	CAGG	AAAG	480
QY	856	TAG	CCCA	CAGG	CCAT	CTG	TGA	CTC	CGG	CCCT	CCG	TGCC	ATAG	915
DB	481	TAG	CCCA	CAGG	CCAT	CTG	TGA	CTC	CGG	CCCT	CCG	TGCC	ATAG	540
QY	916	GCC	CTTCT	TAG	CAT	GA	GTGTG	TGG	GGA	TTTG	CAG	AA	CA	975
DB	541	GCC	CTTCT	TAG	CAT	GA	GTGTG	TGG	GGA	TTTG	CAG	AA	CA	600
QY	976	AAT	CTAGG	ATTATT	CA	AA	CA	AA	AGG	1001				
DB	601	AAT	CTAGG	ATTATT	CA	AA	CA	AA	AGG	626				

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RESULT 15
US-10-027-632-134480
; Sequence 134480, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCES: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 134480  
; LENGTH: 683  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-134480

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Query Match          62.5%; Score 625.6; DB 6; Length 683;
Best Local Similarity 99.8%; Pred. No. 3.4e-194;
Matches 625; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 376 GGGGCTACTGCGACGACCTTTTACTAAAGCCAGTTCTCTGGTTCTGATGATGATGCTCA 435
Db 1 GGGGCTACTGCGACGACCTTTTACTAAAGCCAGTTCTCTGGTTCTGATGATGCTCA 60
QY 436 GTTATGGGAGACTTAACATAGGGAGTGGGGATGGGGAAACCCGGAGGCTGCGCATCTT 495
Db 61 GTTATGGGAGACTTAACATAGGGAGTGGGGATGGGGAAACCCGGAGGCTGCGCATCTT 120
QY 496 TGCATGCCCGAGTGTCTTGGGAGGATAATGCTCTAGAGATGCCACGCTCTGATTCCTC 555
Db 121 TGCATGCCCGAGTGTCTTGGGAGGATAATGCTCTAGAGATGCCACGCTCTGATTCCTC 180
QY 556 CCMAACTGTGACAGAACCCGCCGCCGCCAGGGCTTTGACGATGATCTCCGTGAG 615
Db 181 CCMAACTGTGACAGAACCCGCCGCCGCCAGGGCTTTGACGATGATCTCCGTGAG 240
QY 616 GACCTGTAGGTCTTGGGATCCTTCGGGACTACCTGCAGGCCCGAAAGTAATCCAGGGTT 675
Db 241 GACCTGTAGGTCTTGGGATCCTTCGGGACTACCTGCAGGCCCGAAAGTAATCCAGGGTT 300
QY 676 CTGGGAAGAGCGGGCAGAGGGTTCAGAGGGGGCAGCCTCAGGACGATGGAGGCAGTCA 735
Db 301 CTGGGAAGAGCGGGCAGAGGGTTCAGAGGGGGCAGCCTCAGGACGATGGAGGCAGTCA 360
QY 736 GTCTGAGGCTGAAAAGGAGGAGGGCTTCGAGCCCGAGCCTGCAAGCGCTTCCAGAAAGC 795
Db 361 GTCTGAGGCTGAAAAGGAGGAGGGCTTCGAGCCCGAGCCTGCAAGCGCTTCCAGAAAGC 420
QY 796 TGGMAAAGCGGGAGGAGCCCTCCAGGAGCTGACAGAGGAGGACCGCTGGCCCT 855
Db 421 TGGMAAAGCGGGAGGAGCCCTCCAGGAGCTGACAGAGGAGGACCGCTGGCCCT 480
QY 856 TAGCCACCGAGGGCCCATCGTGGACCTCCGGCTCCGTGCCATAGGAGGCACTCGCGCT 915
Db 481 TAGCCACCGAGGGCCCATCGTGGACCTCCGGCTCCGTGCCATAGGAGGCACTCGCGCT 540
QY 916 GCCCTTCTAGCATGAAAGTGTGTGGGATTTGAGAGCAACAGGAAACCCATGCACTGTG 975
Db 541 GCCCTTCTAGCATGAAAGTGTGTGGGATTTGAGAGCAACAGGAAACCCATGCACTGTG 600
QY 976 AATCTAGGATTTTCAAAACAAAGG 1001
Db 601 AATCTAGGATTTTCAAAACAAAGG 626
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Search completed: January 10, 2006, 20:35:08  
Job time : 951.333 secs

## SUMMARIES

241 GGCATCTCAAGGGAATTACGCTGAGTCAAAACTGCCACCCTCCATGGGATACGTA

	Query Match	100.0%;	Score 1001;	DB 3;	Length 15418;
	Best Local Similarity	100.0%;	Prod. No. 0;		
	Matches 1001;	Conservative	0;	Mismatches	0; Indels
					0; Gaps
Qy	1	AAAGACCCAGCATTTGGCACCCTCTGGACATTTGGCCACAGCCCTCGGGAATTTACAGTGAC	60		
Db	9500	AAAGACCCAGCATTTGGCACCCTCTGGACATTTGGCCACAGCCCTCGGGAATTTACAGTGAC	9559		
Qy	61	TACGCACATCATGTACACACATCTCCCGTCCACGACGACCCCGCTGTTTTATTTTAATAGC	120		
Db	9560	TACGCACATCATGTACACACATCTCCCGTCCACGACGACCCCGCTGTTTTATTTTAATAGC	9619		
Qy	121	TACAAAGCAGGGAAATCCCTGCTTAATATGTCCTTTACAAACCTGGTTAAACAAACGGGTC	180		
Db	9620	TACAAAGCAGGGAAATCCCTGCTTAATATGTCCTTTAAACAACTGGTTAAACAAACGGGTC	9679		
Qy	181	CATCCGCAACGGTGGACAGTTTCTCTCACAGTGAAGAGGAACATGCCGTTTTATAAGCCCTGCA	240		
Db	9680	CATCCGCAACGGTGGACAGTTTCTCTCACAGTGAAGAGGAACATGCCGTTTTATAAGCCCTGCA	9739		
Qy	241	GGCATCTCAAGGGGAATTAAGCTTGAGTCAAAACTGGCACTCTCCATGGGATACGTACGCACAC	300		

Db 9740 GGCAATCTCAAGGGGAATTACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 9799  
Qy 301 ATGCTCAAAAGAAAGAAATTTACCCATGACGAGGAGTGGTTGGGGGTTAAGGACGG 360  
Db 9800 ATGCTCAAAAGAAAGAAATTTACCCATGACGAGGAGTGGTTGGGGGTTAAGGACGG 9859  
Qy 361 TGGGGGACGACGCTGGGGGCTACTGACGACCTTTTAAAGCCAGTTTCTGGTTCT 420  
Db 9860 TGGGGGACGACGCTGGGGGCTACTGACGACCTTTTAAAGCCAGTTTCTGGTTCT 9919  
Qy 421 GATGGATTGGCTCAGTATGGGAGACTAAACATAGGGGAGTGGGGAGGAGCCCG 480  
Db 9920 GATGGATTGGCTCAGTATGGGAGACTAAACATAGGGGAGTGGGGAGGAGCCCG 9979  
Qy 481 AGGCTGGCCATCTTCCCATGCCCCGAGTCTCCGAGTCTGGGAGTGGGAGTGGC 540  
Db 9980 AGGCTGGCCATCTTCCCATGCCCCGAGTCTCCGAGTCTGGGAGTGGGAGTGGC 10039  
Qy 541 CAGCTCTGATTTCCCAAACTGTGACAGAAACCCCGCCCGCCAGGGCCTTTGACG 600  
Db 10040 CAGCTCTGATTTCCCAAACTGTGACAGAAACCCCGCCCGCCAGGGCCTTTGACG 10099  
Qy 601 TGTGATCTCCGTGAGGACCTGAGGTTGGGATCTGGGATCTTCCGAGCTACCTG 660  
Db 10100 TGTGATCTCCGTGAGGACCTGAGGTTGGGATCTGGGATCTTCCGAGCTACCTG 10159  
Qy 661 AGTAATCCAGGGTTCTGGGAAGAGCGGCGAGAGGTTGAGGGGGGAGGCTCAGGA 720  
Db 10160 AGTAATCCAGGGTTCTGGGAAGAGCGGCGAGAGGTTGAGGGGGGAGGCTCAGGA 10219  
Qy 721 CGATGGAGGAGTCACTGAGGCTGAAAGAGGAGGAGGAGGCTCCAGGCGCCAGGCTGCA 780  
Db 10220 CGATGGAGGAGTCACTGAGGCTGAAAGAGGAGGAGGAGGCTCCAGGCGCCAGGCTGCA 10279  
Qy 781 AGCGCTCCAGAGCTGGAAAAAGCGGGAGGAGACCTCCAGGAGCCTGACAGAGGAA 840  
Db 10280 AGCGCTCCAGAGCTGGAAAAAGCGGGAGGAGAGGAGCCTCCAGGAGCCTGACAGAGGAA 10339  
Qy 841 GGACGGCTGGCCCTTAGCCACGAGGCGCCATCGTGAGCTCCGGCTCCGTCGCATAG 900  
Db 10340 GGACGGCTGGCCCTTAGCCACGAGGCGCCATCGTGAGCTCCGGCTCCGTCGCATAG 10399  
Qy 901 GAGGGCACTCGCTGCTGCTTAGCATGAAGTGTGGGGATTGACAGAGCAACAGGA 960  
Db 10400 GAGGGCACTCGCTGCTGCTTAGCATGAAGTGTGGGGATTGACAGAGCAACAGGA 10459  
Qy 961 AACCCATGCACTGTGAATCTAGGATTATTTCAAAACAAAGG 1001  
Db 10460 AACCCATGCACTGTGAATCTAGGATTATTTCAAAACAAAGG 10500

RESULT 2

US-09-994-427A-1  
; Sequence 1, Application US/09994427A  
; Patent No. US20020128221A1  
; GENERAL INFORMATION:  
; APPLICANT: Geron Corporation  
; APPLICANT: Schiff, J. Michael  
; TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER  
; FILE REFERENCE: 083,002  
; CURRENT APPLICATION NUMBER: US/09/994,427A  
; CURRENT FILING DATE: 2002-02-26  
; PRIOR APPLICATION NUMBER: 60/253,395  
; PRIOR FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 15418  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-994-427A-1

Query Match

100.0%; Score 1001; DB 3; Length 15418;

RESULT 3

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAAAGAGCCAGCAATTTGGCAGCCCTGGACATTTGCCCCCAGAGCCCTGGGAATTCACGTGAC 60  
Db 9500 AAAAGAGCCAGCAATTTGGCAGCCCTGGCAGATTTGCCCCCAGAGCCCTGGGAATTCACGTGAC 9559  
Qy 61 TAGCGCATCATCATGTACACATCTCCCGTCCAGCAGCAGCAGCCCGCTGTTTATTTTAAATAGC 120  
Db 9560 TAGCGCATCATCATGTACACATCTCCCGTCCAGCAGCAGCAGCCCGCTGTTTATTTTAAATAGC 9619  
Qy 121 TACAAGAGCAGGGAATTCCTGCTAAATATGCTTTAAACAACTGGTTTAAACAAACCGGTC 180  
Db 9620 TACAAGAGCAGGGAATTCCTGCTAAATATGCTTTTAAACAACTGGTTTAAACAAACCGGTC 9679  
Qy 181 CATCCGACGCTGGAAGTTCCTCAAGTGAAGAGAAACATGCGTTTATTAAGACCTGCA 240  
Db 9680 CATCCGACGCTGGAAGTTCCTCAAGTGAAGAGAAACATGCGTTTATTAAGACCTGCA 9739  
Qy 241 GGCATCTCAAGGGAATTTACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 300  
Db 9740 GGCATCTCAAGGGAATTTACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 9799  
Qy 301 ATGCTCAAAAGAAAGAAATTTACCCCATGCGAGGAGTGGTTGGGGGTTAAGGACGG 360  
Db 9800 ATGCTCAAAAGAAAGAAATTTACCCCATGCGAGGAGTGGTTGGGGGTTAAGGACGG 9859  
Qy 361 TGGGGGACGACGCTGGGGGCTACTGACGACCTTTTAAAGCCAGTTTCTGGTTCT 420  
Db 9860 TGGGGGACGACGCTGGGGGCTACTGACGACCTTTTAAAGCCAGTTTCTGGTTCT 9919  
Qy 421 GATGGATTGGCTCAGTATGGGAGACTAAACATAGGGGAGTGGGGAGGAGCCCG 480  
Db 9920 GATGGATTGGCTCAGTATGGGAGACTAAACATAGGGGAGTGGGGAGGAGCCCG 9979  
Qy 481 AGGCTGTGCCATCTTTGCCATGCGGAGTCTCGGAGTCTTCCGAGTCTTACAGATGCC 540  
Db 9980 AGGCTGTGCCATCTTTGCCATGCGGAGTCTCGGAGTCTTCCGAGTCTTACAGATGCC 10039  
Qy 541 CAGCTCTGATTTCCCAAACTGTGACAGAAACCCCGCCCGCCAGGGCCTTTGACG 600  
Db 10040 CAGCTCTGATTTCCCAAACTGTGACAGAAACCCCGCCCGCCAGGGCCTTTGACG 10099  
Qy 601 TGTGATCTCCGTGAGGACCTGAGGTTGGGATCTGGGATCTTCCGAGCTACCTGACAGCCCGGAAA 660  
Db 10100 TGTGATCTCCGTGAGGACCTGAGGTTGGGATCTGGGATCTTCCGAGCTACCTGACAGCCCGGAAA 10159  
Qy 661 AGTAATCCAGGGTTCTGGGAAGAGCGGCGAGAGGTTGAGGGGGGAGGCTCAGGA 720  
Db 10160 AGTAATCCAGGGTTCTGGGAAGAGCGGCGAGAGGTTGAGGGGGGAGGCTCAGGA 10219  
Qy 721 CGATGGAGGAGTCACTGAGGCTGAAAGAGGAGGAGGAGGCTCCAGGCGCCAGGCTGCA 780  
Db 10220 CGATGGAGGAGTCACTGAGGCTGAAAGAGGAGGAGGAGGCTCCAGGCGCCAGGCTGCA 10279  
Qy 781 AGCGCTCCAGAGCTGGAAAAAGCGGGAGGAGACCTCCAGGAGCCTGACAGAGGAA 840  
Db 10280 AGCGCTCCAGAGCTGGAAAAAGCGGGAGGAGAGGAGCCTCCAGGAGCCTGACAGAGGAA 10339  
Qy 841 GGACGGCTGGCCCTTAGCCACGAGGCGCCATCGTGAGCTCCGGCTCCGTCGCATAG 900  
Db 10340 GGACGGCTGGCCCTTAGCCACGAGGCGCCATCGTGAGCTCCGGCTCCGTCGCATAG 10399  
Qy 901 GAGGGCACTCGCTGCTGCTTAGCATGAAGTGTGGGGATTGACAGAGCAACAGGA 960  
Db 10400 GAGGGCACTCGCTGCTGCTTAGCATGAAGTGTGGGGATTGACAGAGCAACAGGA 10459  
Qy 961 AACCCATGCACTGTGAATCTAGGATTATTTCAAAACAAAGG 1001  
Db 10460 AACCCATGCACTGTGAATCTAGGATTATTTCAAAACAAAGG 10500



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 05:46:59 ; Search time 690.667 Seconds  
(without alignments)  
9659.301 Million cell updates/sec

Title: US-09-615-039-1\_COPY\_9500\_10500  
Perfect score: 1001  
Sequence: 1 aaagaccagcattgac.....ggattattcaaaacaaagg 1001

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- N Geneseq 21:\*
- 1: geneseqn1980s:\*
  - 2: geneseqn1908s:\*
  - 3: geneseqn2000s:\*
  - 4: geneseqn2001as:\*
  - 5: geneseqn2001bs:\*
  - 6: geneseqn2002as:\*
  - 7: geneseqn2002bs:\*
  - 8: geneseqn2003as:\*
  - 9: geneseqn2003bs:\*
  - 10: geneseqn2003cs:\*
  - 11: geneseqn2003ds:\*
  - 12: geneseqn2004as:\*
  - 13: geneseqn2004bs:\*
  - 14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1001	100.0	15418	3	Aa63785 Nucleotide
2	1001	100.0	15418	6	Aa138601 Human TER
3	1001	100.0	15418	6	Ab54997 Lambda cl
4	1001	100.0	15418	6	Aa138595 DNA of pl
5	1001	100.0	15418	10	Adc21253 Lambda cl
6	988.4	98.7	5126	2	Aax88272 Human cat
7	988.4	98.7	51552	6	Aax96607 DNA encod
8	940.4	93.9	4356	13	Adv23863 Human hTE
9	914.4	91.3	4293	14	Adv23865 Human hTE
10	869.4	86.9	3962	4	Aa41091 Telomeras
11	598	59.7	4356	6	Ab192334 Chemical
12	535.8	53.5	4356	6	Ab192335 Chemical
13	467.4	46.7	480	8	Ab275670 Human TER
14	371	37.1	5491	13	Adu82631 Human hTE
15	57.6	5.8	467	3	Aa41829 Human sec
16	55	5.5	33737	6	Aa150815 Human can
17	50.2	5.0	223556	11	Acn44110 Human gen
18	50.2	5.0	243428	12	Adf51132 Human P-R
19	49.8	5.0	10732	3	Aa10594 Gene enco

C	20	48.8	4.9	430	5	ABa13896	Abal3896 Human ner
C	21	48.8	4.9	110000	10	ABQ84281_3	Continuation (4 of
C	22	48.6	4.9	1425	5	ABA20632	AbA20632 Human ner
C	23	48	4.8	2000	8	ADA71938	Ada71938 Rice gene
C	24	47.6	4.8	257645	12	ADQ97289	Adq97289 Human can
C	25	46.8	4.7	51719	6	AAD31365	Aad31365 52Kb gene
C	26	46.8	4.7	92139	6	AAD31364	Aad31364 92Kb gene
C	27	46.8	4.7	130320	10	ADF11613	Adf11613 Human scl
C	28	46.2	4.6	191010	12	ADO25291	Ado25291 Human pro
C	29	45.2	4.5	183337	8	ABQ77402	Abq77402 Human BDN
C	30	44.8	4.5	2000	8	ADA71938	Ada71938 Rice gene
C	31	44.8	4.5	12555	4	ABK42300	Abk42300 Genomic s
C	32	44.8	4.5	12555	4	AAK78331	Aak78331 Human imm
C	33	44.8	4.5	12555	9	ADB60456	Adb60456 Connectiv
C	34	44.2	4.4	699	4	AAH92146	Aah92146 Human inf
C	35	43.6	4.4	108316	10	ADC87336	Adc87336 Human GPC
C	36	42.8	4.3	7967	14	ADX44917	Adx44917 Human gal
C	37	42.8	4.3	9821	14	ADX44918	Adx44918 Human gal
C	38	42.8	4.3	10673	14	AEA61130	Aea61130 Human LGA
C	39	42.8	4.3	96256	13	ADR53001	Adr53001 Drug ther
C	40	42.6	4.3	39887	4	AAK81263	Aak81263 Human imm
C	41	42.6	4.3	39887	4	AAK79153	Aak79153 Human imm
C	42	42.2	4.2	66804	6	ABK87050	Abk87050 Human tra
C	43	42.2	4.2	66804	10	ADG88330	Adg88330 Human tra
C	44	41.8	4.2	33352	9	ADA02846	Ada02846 Human FGF
C	45	41.8	4.2	33352	10	ADB72584	Adb72584 Human FGF

ALIGNMENTS

RESULT 1

AAA63785  
ID AAA63785 standard; DNA; 15418 BP.

AC AAA63785;

DT 04-DEC-2000 (first entry)

XX Nucleotide sequence of the human TERT promoter and gene from pGRN142.

DE Telomerase reverse transcriptase; TERT; promoter; telomerase complex;

XX telomere length; hyperplastic disease; cancer; oncolytic virus;

KW cis-acting transcriptional control sequence; viral replication;

KW cell proliferation; aging; immunological disorder; infertility; ss.

XX Homo sapiens.

OS WO200046355-A2.

PN 10-AUG-2000.

PD 04-FEB-2000; 2000WO-US003104.

PF 04-FEB-1999; 99US-00244438.

XX (GERO-) GERON CORP.

XX Morin GB, Lichtsteiner S, Vasserot A, Adams R, Cardozo LM;

XX Lebkowski JS;

XX WPI; 2000-532898/48.

XX New polynucleotides comprising cis-acting transcriptional control

XX sequences, e.g. promoter sequence, of telomerase reverse transcriptase

XX genes, useful in the treatment of cancer.

XX Claim 9; Page 58-61; 63pp; English.

XX The present sequence represents the human telomerase reverse

XX transcriptase (TERT) promoter and gene. TERT is part of the telomerase

XX complex responsible for maintaining telomere length and increasing

XX replicative capacity of progenitor cells. Telomerase activity is turned

off in mature differentiated cells, but is turned back on again in hyperplastic diseases, including many cancers. The polynucleotide comprises cis-acting transcriptional control sequences, e.g. promoter sequences in which a toxin or genetic element essential for viral replication is placed under the control of a TERT promoter. As a result, the virus replicates preferentially in cells expressing TERT, and selectively lyses cancer cells. The oncolytic viruses are useful for treating cancer in humans or animals. The TERT promoter sequences are useful in the treatment of cancer and other diseases of cell proliferation such as degenerative and aging processes and diseases of aging, immunological disorders, or infertility

XX SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 1001; DB 3; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 2.9e-289;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAGACCCAGCATTTGGCACCCCTGGACATTTGCCCCACAGCCCTGGGAATTCACGTGAC 60  
DB 9500 AAAAGACCCAGCATTTGGCACCCCTGGACATTTGCCCCACAGCCCTGGGAATTCACGTGAC 9559

QY 61 TAGCGCATCATGTATACACTCCCGTCCACAGCCGACCCCGCTGTTTATTTAATAGC 120  
DB 9560 TAGCGCATCATGTATACACTCCCGTCCACAGCCGACCCCGCTGTTTATTTAATAGC 9619

QY 121 TACAAGCAGGAAATCCCTGCTAAATGTCCTTTAACAACCTGGTTAAACAACCGGTC 180  
DB 9620 TACAAGCAGGAAATCCCTGCTAAATGTCCTTTAACAACCTGGTTAAACAACCGGTC 9679

QY 181 CATCCGACAGGTGACAGTTCCTCACAGTCAAGAGGAACATGCCGTTTATAAGCCCTGCA 240  
DB 9680 CATCCGACAGGTGACAGTTCCTCACAGTCAAGAGGAACATGCCGTTTATAAGCCCTGCA 9739

QY 241 GGCACTCTCAAGGGAATTTACGCTGAGTCAGTCCAAACTGCCACCTCCATGGGATACGTACGCAAC 300  
DB 9740 GGCACTCTCAAGGGAATTTACGCTGAGTCAGTCCAAACTGCCACCTCCATGGGATACGTACGCAAC 9799

QY 301 ATGCTCAAAAAGAAAGAAATTTCAACCCATGCGAGGGAGTGGTTGGGGGGTTAAGACGG 360  
DB 9800 ATGCTCAAAAAGAAAGAAATTTCAACCCATGCGAGGGAGTGGTTGGGGGGTTAAGACGG 9859

QY 361 TGGGGCAGCAGCTGGGGGCTACTGCACGACCTTTTACTAAGCCAGTTCCTGCTTCT 420  
DB 9860 TGGGGCAGCAGCTGGGGGCTACTGCACGACCTTTTACTAAGCCAGTTCCTGCTTCT 9919

QY 421 GATGGTATTGGCTCAGTTATGGGAGACTAACCACTAGGGGAGTGGGGATGGGGAAACCCGG 480  
DB 9920 GATGGTATTGGCTCAGTTATGGGAGACTAACCACTAGGGGAGTGGGGATGGGGAAACCCGG 9979

QY 481 AGGCTGTGCCATCTTTGCCATGCCCGAGTGTCTTGGGCGAGTAATGCTCTAGAGATGCC 540  
DB 9980 AGGCTGTGCCATCTTTGCCATGCCCGAGTGTCTTGGGCGAGTAATGCTCTAGAGATGCC 10039

QY 541 CAGTCTCTGATTTCCCAACCTGTGCAGACACCCCGCCCGCCCGCCAGGCTTTCAGG 600  
DB 10040 CAGTCTCTGATTTCCCAACCTGTGCAGACACCCCGCCCGCCCGCCAGGCTTTCAGG 10099

QY 601 TGTGATCTCCGTGAGGACCTTGAGGTCTGGGATCTTTCGGGACTACTCTGAGGCGCCGAAA 660  
DB 10100 TGTGATCTCCGTGAGGACCTTGAGGTCTGGGATCTTTCGGGACTACTCTGAGGCGCCGAAA 10159

QY 661 AGTAATCCAGGGTTCTGGGAAGAGCGCGGACAGAGGTCAGAGGGGGGCGAGCTCAGGA 720  
DB 10160 AGTAATCCAGGGTTCTGGGAAGAGCGCGGACAGAGGTCAGAGGGGGGCGAGCTCAGGA 10219

QY 721 CGATGAGGCGAGTCAGTCTCAGGCTGAAGAGGAGGAGGCGCTCGAGCCAGGCTGCA 780  
DB 10220 CGATGAGGCGAGTCAGTCTCAGGCTGAAGAGGAGGAGGCGCTCGAGCCAGGCTGCA 10279

QY 781 AGCGCTCTCAGAAAGTGGAAAAAGCGGGGAAGGACCCCTCCAGGAGCCCTGCAGCAGGAA 840

DB 10280 AGCGCTCTCAGAGCTGGAAAAAGCGGGGAAGGACCCCTCCACGAGCCTGCAGCAGGAA 10339

QY 841 GGCACGGCTGGCCCTTAGCCACACGAGGCCCATCTGTGGACCTCCGGCCTCCGTCGCATAG 900

DB 10340 GGCACGGCTGGCCCTTAGCCACACGAGGCCCATCTGTGGACCTCCGGCCTCCGTCGCATAG 10399

QY 901 GAGGGCACTCGCGCTCCCTTCTTAGCATGAAGTGTGTGGGATTTTCAGAAGCAACAGGA 960

DB 10400 GAGGGCACTCGCGCTCCCTTCTTAGCATGAAGTGTGTGGGATTTTCAGAAGCAACAGGA 10459

QY 961 AACCCATGCACCTGTGAATCTAGGATTTATTTCAAACAAGG 1001

DB 10460 AACCCATGCACCTGTGAATCTAGGATTTATTTCAAACAAGG 10500

RESULT 2  
AAL38601  
ID AAL38601 standard; DNA; 15418 BP.  
XX  
AC AAL38601;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
Human TERT promoter and upstream sequence.  
XX  
DE  
XX  
XX  
KW Cytostatic; glycosyltransferase; tumour; cell-surface carbohydrate;  
KW tissue specific; transcriptional control element; cancer cell;  
KW gene therapy; human TERT; telomerase reverse transcriptase; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200242468-A2.  
XX  
PD 30-MAY-2002.  
XX  
PF 26-NOV-2001; 2001WO-US044306.  
XX  
PR 27-NOV-2000; 2000US-0253395P.  
XX  
PA (GERO-) GERON CORP.  
XX  
PI Schiiff MJ;  
XX  
XX WPI; 2002-479954/51.  
XX  
XX  
PT New polynucleotide encoding glycosyltransferase enzymes including histo  
PT blood group transferase useful for treating conditions associated with  
PT hyperproliferation, such as cancers and other neoplasias.  
XX  
PS Claim 9; Page 17-20; 49pp; English.

XX The invention relates to a polynucleotide comprising an encoding sequence  
CC for a glycosyltransferase, under control of a heterologous tumour  
CC specific or tissue specific transcriptional control element, where  
CC expression of the polynucleotide in a human cell causes the cell to  
CC express a cell-surface carbohydrate determinant to which some or all  
CC humans have a naturally occurring antibody. The polynucleotide of the  
CC invention is useful for killing cancer cells and for preparing a  
CC medication for the treatment of cancer. The polynucleotide sequence of  
CC the invention can be used to treat disorders by gene therapy. This  
CC polynucleotide sequence represents the human TERT (telomerase reverse  
CC transcriptase) promoter and upstream sequence related to the invention  
XX  
SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 1001; DB 6; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 2.9e-289;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAGACCCAGCATTTGGCACCCCTGGACATTTGGCCCAACAGCCCTGGGAATTCACGTGAC 60

DB 9500 AAAAGACCCAGCATTTGGCACCCCTGGACATTTGGCCCAACAGCCCTGGGAATTCACGTGAC 9559

Qy	61	TAGCGCATCATGTACACACTCCCGTTCAGGACCGACCCCGCTGTTTATTTAATAGC	120
Db	9560	TAGCGCATCATGTACACACTCCCGTTCAGGACCGACCCCGCTGTTTATTTAATAGC	9619
Qy	121	TACAAAGCAGGGAATCCCTGCTAAATGTCCTTTAAACAAACTGTGTAAACAAACGGGTC	180
Db	9620	TACAAAGCAGGGAATCCCTGCTAAATGTCCTTTAAACAAACTGTGTAAACAAACGGGTC	9679
Qy	181	CATCCGCACGGTGGACAGTTTCTTCACAGTGAAGAGGAAACATGCCGTTTATAAAGCTGCA	240
Db	9680	CATCCGCACGGTGGACAGTTTCTTCACAGTGAAGAGGAAACATGCCGTTTATAAAGCTGCA	9739
Qy	241	GGCATCTCAAGGGAATTAACGTGAGTCAAAAATGCGCACCTCATGGGATACGTAGCGAAC	300
Db	9740	GGCATCTCAAGGGAATTAACGTGAGTCAAAAATGCGCACCTCATGGGATACGTAGCGAAC	9799
Qy	301	ATGCTCAAAAAGAAAGAAATTTACCCCATCAGCAGGGGAGTGTGTGGGGGTTTAAGACGG	360
Db	9800	ATGCTCAAAAAGAAAGAAATTTACCCCATCAGCAGGGGAGTGTGTGGGGGTTTAAGACGG	9859
Qy	361	TGGGGGCAGCAGCTGGGGGCTACTGACGACACCTTTTACTAAAGCCAGTTTCTCGTTCT	420
Db	9860	TGGGGGCAGCAGCTGGGGGCTACTGACGACACCTTTTACTAAAGCCAGTTTCTCGTTCT	9919
Qy	421	GATGGTATTGGCTCAGTTATGGGAGACTAACCATAGGGAGTGGGGATGGGGAAACCCGG	480
Db	9920	GATGGTATTGGCTCAGTTATGGGAGACTAACCATAGGGAGTGGGGATGGGGAAACCCGG	9979
Qy	481	AGGCTGTGCCATCTTTGGCCATGCCAGTGTCTCTGGGCAGGATATGCTCTAGAGATGCC	540
Db	9980	AGGCTGTGCCATCTTTGGCCATGCCAGTGTCTCTGGGCAGGATATGCTCTAGAGATGCC	10039
Qy	541	CACGTCCTGATTTCCCCAAACCTGTGTGACAGAACCCCGCCCGCCCTTTGCGAGG	600
Db	10040	CACGTCCTGATTTCCCCAAACCTGTGTGACAGAACCCCGCCCGCCCTTTGCGAGG	10099
Qy	601	TGTGATCTCGTGAGGACCCCTGAGGTCCTGGGATCTTTCGGGACTACTCTGAGGCCCGAAA	660
Db	10100	TGTGATCTCGTGAGGACCCCTGAGGTCCTGGGATCTTTCGGGACTACTCTGAGGCCCGAAA	10159
Qy	661	AGTAACTCCAGGGTCTTGGGAAGAGCGCGGACGAGGCTCAGAGGGGGGACGCTCAGGA	720
Db	10160	AGTAACTCCAGGGTCTTGGGAAGAGCGCGGACGAGGCTCAGAGGGGGGACGCTCAGGA	10219
Qy	721	CGATGAGGCAGTCAAGTCTGAGGCTGAAAAGGAGGAGGGGCTCTGAGCCACGGCTGCA	780
Db	10220	CGATGAGGCAGTCAAGTCTGAGGCTGAAAAGGAGGAGGGGCTCTGAGCCACGGCTGCA	10279
Qy	781	AGCGCTCTCAGAAAGCTGAAAAAAGCGGGGAAGGGAACCTTCCACGAGGCTGCAGCAGAA	840
Db	10280	AGCGCTCTCAGAAAGCTGAAAAAAGCGGGGAAGGGAACCTTCCACGAGGCTGCAGCAGAA	10339
Qy	841	GGCAGGCTGGCCCTTAGGCCACGAGGGCCCATCGTGGACCTCCGGCTCCGTCGCATAG	900
Db	10340	GGCAGGCTGGCCCTTAGGCCACGAGGGCCCATCGTGGACCTCCGGCTCCGTCGCATAG	10399
Qy	901	GAGGGCACTCGCGTGCCTTCTTAGCATGAAGTGTGTGGGATTTTGCAGAACCAACAGGA	960
Db	10400	GAGGGCACTCGCGTGCCTTCTTAGCATGAAGTGTGTGGGATTTTGCAGAACCAACAGGA	10459
Qy	961	AACCCATGCACTGTGAATCTAGGATTTATTTCAAAAACAAAGG	1001
Db	10460	AACCCATGCACTGTGAATCTAGGATTTATTTCAAAAACAAAGG	10500

### RESULT 3

RESOL1 3  
ABS54997  
ID ABS54997 standard; DNA; 15418 BP.

XX  
AC  
ABS54997;

XX  
DT 10-DEC-2002 (first entry)

58

Lambda clone containing human TERT genomic insert.

Telomerase reverse transcriptase; TERT; replication-conditional virus; adenovirus replication gene; cancer cell; lung; pancreatic cancer; medulloblastoma; cervical carcinoma; fibrosarcoma; osteosarcoma; cytolytic; replication defective adenovirus vector; congenital defect; proinflammatory; antiinflammatory; heterologous effector gene; cancer therapy; cycostatic; gene therapy; lambda clone; human; ds.

Bacteriophage lambda.

Homo sapiens.

Synthetic.

Key	Location/Qualifiers
misc_feature	1. .43
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	/note= "From Lambda clone"
misc_feature	44. .15375
	/*tag= b
	/note= "Human telomerase reverse transcriptase (hTERT) sequence including the hTERT promoter and upstream sequence"
misc_feature	15376. .15418
	/*tag= c
	/note= "From Lambda clone"

WO200253760-A2.

11-JUL-2002.

17-DEC-2001; 2001WO-US048785.

18-DEC-2000; 2000US-0256418P.

(GERO-) GERON CORP.

Irving JM, Lebkowski JS;

WPI; 2002-723123/78.

Novel replication-conditional virus useful for cytolysis of target cells e.g. cancer cells and preparing a medicament for treating cancer, comprises heterologous replication element in an adenovirus-based construct.

Claim 11; Page 26-29; 32pp; English.

The present invention relates to a new replication-conditional virus with a genome comprising adenovirus replication genes and one or more heterologous gene(s) that functionally replaces one or more adenovirus gene(s) required for replication or assembly of the virus. The invention is useful for killing a cancer cell (such as lung, pancreatic cancer, medulloblastoma, cervical carcinoma, fibrosarcoma or osteosarcoma), killing a cell expressing TERT (telomerase reverse transcriptase), and in preparing a medicament for treating cancer and a condition associated with increased expression of TERT in affected cells, in a subject. The invention is also useful for cytolysis of specific target cells. The invention is further useful for producing replication defective adenovirus vector which is useful for transient expression of a heterologous therapeutic gene to correct a congenital defect, introducing proinflammatory or antiinflammatory activity, enhancing telomerase function, and delivering heterologous effector genes that induce killing of the transduced cells. The invention is more safe for use in cancer therapy. The present nucleic acid sequence represents the human TERT sequence contained within a lambda clone sequence of the invention

Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1001;	DB 6;	Length 15418;
Best Local Similarity	100.0%;	Pred. No. 2.9e-289;		
Matches 1001;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

1 AAAAGACCCAGCAATGGCACCCCTGGACATTTGGCCCCACAGCCCTTGGGAATTCACGTGAC 60

Db	9500	AAAAAGCCCGACATTTGGCACCCCTGGACATTTTGGCCCCACAGGCCCTGGGAAATTCACGTGAC	9559
Qy	61	TACGCACATCATGTACACATCTCCCGTCCAGCACCGACCCCGCTGTTTTATTTAATAGC	120
Db	9560	TACGCACATCATGTACACATCTCCCGTCCAGCACCGACCCCGCTGTTTTATTTAATAGC	9619
Qy	121	TACAAAGCAGGGAATCCCTGCTAAATGCTTTTAACAAACCTGGTTAAACAAACGGGTC	180
Db	9620	TACAAAGCAGGGAATCCCTGCTAAATGCTTTTAACAAACCTGGTTAAACAAACGGGTC	9679
Qy	181	CATCCGACAGGTGGACAGTTTCCTCACAGTGAAGAGGAACATGCCGTTTATAAAGCTCGCA	240
Db	9680	CATCCGACAGGTGGACAGTTTCCTCACAGTGAAGAGGAACATGCCGTTTATAAAGCTCGCA	9739
Qy	241	GGCATCTCAAGGGAATTAAGCTGAGTCAAAACCTGCCACCTCATGGGATACGTACGCAAC	300
Db	9740	GGCATCTCAAGGGAATTAAGCTGAGTCAAAACCTGCCACCTCATGGGATACGTACGCAAC	9799
Qy	301	ATGCTCAAAAGAAAGAAATTTTCAACCCCATGGCAGGGAGTGCTGGGGGTTTAAGGACGG	360
Db	9800	ATGCTCAAAAGAAAGAAATTTTCAACCCCATGGCAGGGAGTGCTGGGGGTTTAAGGACGG	9859
Qy	361	TGGGGGCAGCAGCTGGGGGCTACTGCAACGACCTTTTACTAAAGCCAGTTTCTCGTGTCT	420
Db	9860	TGGGGGCAGCAGCTGGGGGCTACTGCAACGACCTTTTACTAAAGCCAGTTTCTCGTGTCT	9919
Qy	421	GATGGTATTGGCTCAGTTATGGGAGACTAAACCATAGGGGAGTGGGGATGGGGGAACCCGG	480
Db	9920	GATGGTATTGGCTCAGTTATGGGAGACTAAACCATAGGGGAGTGGGGATGGGGGAACCCGG	9979
Qy	481	AGGCTGTGCCATCTTTGGCCATGCCCAGTGTCTGGGCAGGATAATGCTTAGAGATGCC	540
Db	9980	AGGCTGTGCCATCTTTGGCCATGCCCAGTGTCTGGGCAGGATAATGCTTAGAGATGCC	10039
Qy	541	CAGCTCTGATTTCCCCAAACCTGTGGACAGAACCCGCCGCCGCCAGGCTTTTGCAGG	600
Db	10040	CAGCTCTGATTTCCCCAAACCTGTGGACAGAACCCGCCGCCGCCAGGCTTTTGCAGG	10099
Qy	601	TGTGATCTCCGTGAGGACCTGAGGCTCGGATCTTGGGACTACCTGCGAGGCCCGAAA	660
Db	10100	TGTGATCTCCGTGAGGACCTGAGGCTCTGGATCTTTCGGACTTACCTGAGGCCCCGAAA	10159
Qy	661	AGTAATCCAGGGTTCTGGGAAGAGCGGCGCAGGAGGTTCAGAGGGGGCAGCCTCAGGA	720
Db	10160	AGTAATCCAGGGTTCTGGGAAGAGCGGCGCAGGAGGTTCAGAGGGGGCAGCCTCAGGA	10219
Qy	721	CGATGGAGCAGTCACTCTGAGGCTGAAAGGGAGGGGCGCTCGAGCCCGAGGCTCGA	780
Db	10220	CGATGGAGCAGTCACTCTGAGGCTGAAAGGGAGGGGCGCTCGAGCCCGAGGCTCGA	10279
Qy	781	AGCGCTTCCAGAAAGTGGAAAAGCGGGGAAGGGACCTTCCAGCGAGCTCGCAGCAGGAA	840
Db	10280	AGCGCTTCCAGAAAGTGGAAAAGCGGGGAAGGGACCTTCCAGCGAGCTCGCAGCAGGAA	10339
Qy	841	GGCAGGCTGGCCCTTAGCCCAACAGGGCCCATCTGTGGACCTCCGGCTCTCGTGCCATAG	900
Db	10340	GGCAGGCTGGCCCTTAGCCCAACAGGGCCCATCTGTGGACCTCCGGCTCTCGTGCCATAG	10399
Qy	901	GAGGGCACTCGGCTGCCTTCTTAGCATCAAGTGTGTGGGATTTTGCAGAGCAACAGGA	960
Db	10400	GAGGGCACTCGGCTGCCTTCTTAGCATCAAGTGTGTGGGATTTTGCAGAGCAACAGGA	10459
Qy	961	AACCCATGCACTGTGAATCTAGGATTTATTTCAAAAACAAAGG	1001
Db	10460	AACCCATGCACTGTGAATCTAGGATTTATTTCAAAAACAAAGG	10500

RESULT 4  
AAL38595  
ID AAL  
XX  
AC AAL

XX	16-AUG-2002	(first entry)
DT		
XX		
XX		
DE		DNA of plasmid pGERN144 containing human hTERT gene.
XX		
XX		Anticonvulsant; cerebroprotective; vasotropic; neurotropic; stem cell;
KW		neuroprotective; antiparkinsonian; antiinflammatory; undifferentiated;
KW		cardiant; transcriptional control element; human embryonic; tissue graft;
KW		regenerative medicine; tissue reconstitution; neural progenitor cell;
KW		nerve system; epilepsy; stroke; ischaemia; Huntington's disease;
KW		Parkinson's disease; multiple sclerosis; leukodystrophy; neuritis;
KW		hepatocyte; liver damage; cardiomyocyte; cryoinjury; cardiac muscle;
KW		pGERN144; human hTERT gene; chimeric; ds.
XX		
OS		Homo sapiens.
OS		Unidentified.
OS		Chimeric.
XX		
XX		WO2002424445-A2.
XX		
PD		30-MAY-2002.
XX		
XX		26-NOV-2001; 2001WO-US044309.
XX		
XX		27-NOV-2000; 2000US-0253357P.
PR		27-NOV-2000; 2000US-0253443P.
PR		13-FEB-2001; 2001US-00783203.
XX		
XX		(GERO-) GERON CORP.
PA		
XX		
XX		Gold JD, Lebrowski JS;
FI		
XX		WPI; 2002-479952/51.
DR		
XX		
XX		Depleting a cell e.g., human embryonic stem cell population of
PT		undifferentiated stem cells (UC) for use in regenerative medicine
PT		comprises genetically altering UC in a population to express nucleic acid
PT		encoding a lethal product.

Example 9; Page 62-66; 67pp; English.

The invention relates to a system for depleting a cell population of undifferentiated stem cells, by introducing nucleic acids of structure P-X, where X is a nucleic acid encoding product that is lethal to a cell in which it is expressed; or renders a cell in which it is expressed susceptible to the lethal effect of an external agent, and P is a transcriptional control element causing X to be preferentially expressed in the undifferentiated stem cells. The system is used for depleting a cell population (preferably, human embryonic stem cells) of undifferentiated stem cells. A population of differentiated cells is useful in regenerative medicine, and for preparing antibodies and cDNA libraries that are specific for a differentiated phenotype. The cell populations are also useful for drug screening and therapeutic applications. The differentiated cells are useful for tissue reconstitution or regeneration in a human patient in need of treatment. The cells are administered in a manner that permits to graft to the intended tissue side and reconstitute or regenerate the functionally deficient area. The neural progenitor cells are useful for treating acute or chronic damage to the nerve system e.g. epilepsy, stroke, ischaemia, Huntington's disease, Parkinson's disease, multiple sclerosis, leukodystrophies, neuritis, etc. The hepatocytes and hepatocyte precursors are useful for assessing animal models for ability to repair liver damage. The cardiomyocyte population is useful for assessing animal models for cryoinjury, regenerating cardiac muscle and to treat insufficient cardiac function. This polynucleotide sequence represents the DNA of plasmid pGRN144 containing the human hTERT gene relating to the invention

SQ Sequence 15418 BP; 4519 A; 3797 C; 3764 G; 3338 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1001;	DB 6;	Length 15418;
Best Local Similarity	100.0%;	Pred. No. 2.9e-289;		
Matches 1001;	Conservative 0;	Mismatches 0;	Indels 0;	



```
QY 61 TAGCACATCATGTACACACTCCGCTCCACGACGACCCCGCTGTTTATTTTAAATAGC 120
Db 9560 TAGCACATCATGTACACACTCCGCTCCACGACGACCCCGCTGTTTATTTTAAATAGC 9619
QY 121 TACAAAGCAGGAAATCCCTGCTTAAATGCTCTTAAACAACTGGTTTAAACAAACGGGTC 180
Db 9620 TACAAAGCAGGAAATCCCTGCTTAAATGCTCTTAAACAACTGGTTTAAACAAACGGGTC 9679
QY 181 CATCCGACCGTGGACAGTTCCTCACAGTGAAGAGGAACATGCGCTTTTATAAAGCCCTGCA 240
Db 9680 CATCCGACCGTGGACAGTTCCTCACAGTGAAGAGGAACATGCGCTTTTATAAAGCCCTGCA 9739
QY 241 GGCATCTCAAGGGAATTAACGCTGAGTCAAACTGCGCACCTCCATGGGATAGTACGCAAC 300
Db 9740 GGCATCTCAAGGGAATTAACGCTGAGTCAAACTGCGCACCTCCATGGGATAGTACGCAAC 9799
QY 301 ATGCTCAAAAAGAAATTTACCCCATGCGAGGGGAGTGGTTGGGGGTTAAGGACGG 360
Db 9800 ATGCTCAAAAAGAAATTTACCCCATGCGAGGGGAGTGGTTGGGGGTTAAGGACGG 9859
QY 361 TGGGGGACGAGCTGGGGGCTACTGCAACGACCTTTTACTAAAGCCAGTTTCTGTTCT 420
Db 9860 TGGGGGACGAGCTGGGGGCTACTGCAACGACCTTTTACTAAAGCCAGTTTCTGTTCT 9919
QY 421 GATGCTATGCTCAGTTATGGGAGACTAACATAGGGGAGTGGGGATGGGGGAACCCGG 480
Db 9920 GATGCTATGCTCAGTTATGGGAGACTAACATAGGGGAGTGGGGATGGGGGAACCCGG 9979
QY 481 AGGCTGTGCCATCTTTGCCATGCCAGTGTCTTGGGACGATAATGCTCTAGAGATGCC 540
Db 9980 AGGCTGTGCCATCTTTGCCATGCCAGTGTCTTGGGACGATAATGCTCTAGAGATGCC 10039
QY 541 CAGCTCTGATTCCTCCCAACCTGTGTGACAGAAACCCCGCCGCCCCCAGGGCCCTTTGACGG 600
Db 10040 CAGCTCTGATTCCTCCCAACCTGTGTGACAGAAACCCCGCCGCCCCCAGGGCCCTTTGACGG 10099
QY 601 TGTGATCTCGTAGGACCTGTAGTGTGGGATCTCTGGGACTACTGTGAGGCCGGA 660
Db 10100 TGTGATCTCGTAGGACCTGTAGTGTGGGATCTCTGGGACTACTGTGAGGCCGGA 10159
QY 661 AGTAATCCAGGGTTCTGGGAAGAGGCGGACGAGGGGTGAGAGGGGGGAGCCTCAGGA 720
Db 10160 AGTAATCCAGGGTTCTGGGAAGAGGCGGACGAGGGGTGAGAGGGGGGAGCCTCAGGA 10219
QY 721 CGATGGAGGAGTCACTGAGGCTGAAAAGGAGGAGGGGCTTCGAGCCCGAGGCTGCA 780
Db 10220 CGATGGAGGAGTCACTGAGGCTGAAAAGGAGGAGGGGCTTCGAGCCCGAGGCTGCA 10279
QY 781 AGCGCTCCAGAGCTGGAAAAAAGCGGGGAAGGACCTTCCAGGAGCCTTGACGAGGAA 840
Db 10280 AGCGCTCCAGAGCTGGAAAAAAGCGGGGAAGGACCTTCCAGGAGCCTTGACGAGGAA 10339
QY 841 GGCACGGCTGGCCTTAGCCACGAGGCCCATCGTGAGCTCCGGCTCCGTCCTAG 900
Db 10340 GGCACGGCTGGCCTTAGCCACGAGGCCCATCGTGAGCTCCGGCTCCGTCCTAG 10399
QY 901 GAGGGCAGCTCGCGTGCCTTTCTAGCATGAAGTGTGTGGGGATTTGACAGAGCAACAGGA 960
Db 10400 GAGGGCAGCTCGCGTGCCTTTCTAGCATGAAGTGTGTGGGGATTTGACAGAGCAACAGGA 10459
QY 961 AACCCATGCACTGTGAATCTAGGATTTATTTCAAAACAAAGG 1001
Db 10460 AACCCATGCACTGTGAATCTAGGATTTATTTCAAAACAAAGG 10500
```

## RESULT 6

ID AAX88272 standard; DNA; 5126 BP.

XX AC

XX AC

XX AC

DT 22-SEP-1999 (first entry)

```
XX Human catalytic telomerase subunit 5'-flanking regulatory DNA.
DE Telomerase; subunit; human; regulatory; catalytic; anti-tumour; reporter;
KW modulator; telomerase regulatory region; cancer therapy; ss.
XX Homo sapiens.
OS DE19757984-Al.
PN 01-JUL-1999.
XX 24-DEC-1997; 97DE-01057984.
PF 24-DEC-1997; 97DE-01057984.
XX (FARB ) BAYER AG.
XX Hagen G, Wick M, Zubov D;
PI WPI; 1999-372320/32.
XX New 5' flanking regulatory sequence from the human catalytic telomerase
subunit gene useful for cancer therapy.
XX Claim 1; Fig 4; 14pp; German.
XX This invention describes a novel 5' flanking regulatory sequence from the
human catalytic telomerase subunit gene. Recombinant constructs
containing the product of the invention can be linked with DNA encoding
an anti-tumour protein or reporter protein. The constructs are useful for
identifying candidate substances that modulate the activity of the
telomerase regulatory region. The constructs can be used in cancer
therapy
XX Sequence 5126 BP; 1009 A; 1532 C; 1404 G; 1180 T; 0 U; 1 Other;
```

Query Match 98.7%; Score 988.4; DB 2; Length 5126;  
Best Local Similarity 99.8%; Pred. No. 1.1e-285;  
Matches 1000; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
QY 1 AAAAGACCCAGCATTGGCACCCCTGGACATTTGCCCCACAGCCCTGGGAATTCACGTCAC 60
Db 1079 AAAAGACCCAGCATTGGCACCCCTGGACATTTGCCCCACAGCCCTGGGAATTCACGTCAC 1138
QY 61 TAGGCACATCATGTACACACTCCGCTCCACGACCCCGCTGTTTATTTTAAATAGC 120
Db 1139 TAGGCACATCATGTACACACTCCGCTCCACGACCCCGCTGTTTATTTTAAATAGC 1198
QY 121 TACAAAGCAGGAAATCCCTGCTTAAATGCTCTTTTAAACAACTGGTTTAAACAAACGGGTC 180
Db 1199 TACAAAGCAGGAAATCCCTGCTTAAATGCTCTTTTAAACAACTGGTTTAAACAAACGGGTC 1258
QY 181 CATCCGACCGTGGACAGTTCCTCACAGTGAAGAGGAACATGCGCTTTTATAAAGCCCTGCA 240
Db 1259 CATCCGACCGTGGACAGTTCCTCACAGTGAAGAGGAACATGCGCTTTTATAAAGCCCTGCA 1318
QY 241 GGCATCTCAAGGGAATTAACGCTGAGTCAAACTGCGCACCTCCATGGGATAGTACGCAAC 300
Db 1319 GGCATCTCAAGGGAATTAACGCTGAGTCAAACTGCGCACCTCCATGGGATAGTACGCAAC 1378
QY 301 ATGCTCAAAAAGAAATTTACCCCATGCGAGGGGAGTGGTTTGGGGGTTTAAAGACG 359
Db 1379 ATGCTCAAAAAGAAATTTACCCCATGCGAGGGGAGTGGTTTAAAGACG 1438
QY 360 GTGGGGGACGAGCTGGGGGCTACTGACGACCTTTTACTAAAGCCAGTTTCTGCTGTC 419
Db 1439 GTGGGGGACGAGCTGGGGGCTACTGACGACCTTTTACTAAAGCCAGTTTCTGCTGTC 1498
QY 420 TGAATGTTATTTGGCTCAGTTTATGGGAGACTAAACCATAGGGGAGTGGGGATCGGGGAACCCG 479
Db 1499 TGAATGTTATTTGGCTCAGTTTATGGGAGACTAAACCATAGGGGAGTGGGGATCGGGGAACCCG 1558
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XX	WO2004099377-A2.	QY	48	GAATTCACGTGACATCGCAATCATGTACACATCCCGTCCACGACCGACCCCGCTGTT	107
PN		DB	1	GAATTCACGTGACATCGCAATCATGTACACATCCCGTCCACGACCGACCCCGCTGTT	60
XX	18-NOV-2004.	QY	108	TTATTTTAATAGCTACAAAGCAGGGAATCCCTGCTAAATGTCCTTTAAACAATGTT	167
XX	30-APR-2004; 2004WO-US013487.	DB	61	TTATTTTAATAGCTACAAAGCAGGGAATCCCTGCTAAATGTCCTTTAAACAATGTT	120
XX	01-MAY-2003; 2003US-0467171P.	QY	168	AAACAAACGGGTCCATCCGACCGGTGACAGATTCCTCACAGTGAAGAGGAACATGCCGTT	227
XX	(MUSC-) MUSC FOUND RES DEV.	DB	121	AAACAAACGGGTCCATCCGACCGGTGACAGATTCCTCACAGTGAAGAGGAACATGCCGTT	180
XX	Dong J, Rubinchik S, Woraratanadham J;	QY	228	TATAAAGCCTGACAGGCAATCTCAAGGGAATACGCTGAGTCAAAATCTGCACCTCATGCGG	287
XX	WPI; 2004-805118/79.	DB	181	TATAAAGCCTGACAGGCAATCTCAAGGGAATACGCTGAGTCAAAATCTGCACCTCATGCGG	240
XX	P-PSDB; ADU82634.	QY	288	ATAGCTACGCAACATGCTCAAAAGAAAGAAATTTTCAACCCATGCGAGGAGTGGTGGG	347
XX	GENBANK; AF097365.	DB	241	ATAGCTACGCAACATGCTCAAAAGAAAGAAATTTTCAACCCATGCGAGGAGTGGTGGG	299
XX	New expression vector comprising a first expression cassette with a first	QY	348	GGGTAAAGGACGGTGGGGGCGAGCAGCTGGGGGCTACTGCGACGACCTTTTAAAGCCA	407
XX	coding region that encodes a transcriptional activating factor (TAF),	DB	300	GGGTAAAGGACGGTGGGGGCGAGCAGCTGGGGGCTACTGCGACGACCTTTTAAAGCCA	359
XX	useful in treating cancer, AIDS, hemophilia, diabetes and asthma.	QY	408	GTTCCTCTGCTGATGATGCTTATGGCTCAGTTATGGGAGACTAAACATAGGAGGAGTGGGA	467
XX	Disclosure; SEQ ID NO 5; 112pp; English.	DB	360	GTTCCTCTGCTGATGATGCTTATGGCTCAGTTATGGGAGACTAAACATAGGAGGAGTGGGA	419
XX	The invention relates to an expression vector comprising a first	QY	468	TGGGGAAACCGGAGGCTGTCATCTTTGCAATCCCGAGTGTCTCTGGGAGGATATG	527
XX	expression cassette having a first coding region that encodes a	DB	420	TGGGGAAACCGGAGGCTGTCATCTTTGCAATCCCGAGTGTCTCTGGGAGGATATG	479
XX	transcriptional activating factor (TAF), and a second expression cassette	QY	528	CTCTAGAGATGCCACGCTCTGATTTCCCGCAAACTGTGACAGAACCCCGCCGCCCA	587
XX	comprising a second coding region that encodes a selected polypeptide.	DB	480	CTCTAGAGATGCCACGCTCTGATTTCCCGCAAACTGTGACAGAACCCCGCCGCCCA	539
XX	The expression vector further comprises a first expression cassette	QY	588	GGGCTTTTGCAGGTGTGATCTCTCGTGAGGACCTCTGAGTCTGAGGATCTCTCGGACTACC	647
XX	having a first coding region that encodes a transcriptional activating	DB	540	GGGCTTTTGCAGGTGTGATCTCTCGTGAGGACCTCTGAGTCTGAGGATCTCTCGGACTACC	599
XX	factor (TAF), the first coding region being positioned under the	QY	648	TGCAGGCCCGGAAAGTATTCAGGGGTTCTGGGAAAGGCGGCGAGGAGGCTCAGAGGGG	707
XX	transcriptional control of a first promoter comprising a tissue specific	DB	600	TGCAGGCCCGGAAAGTATTCAGGGGTTCTGGGAAAGGCGGCGAGGAGGCTCAGAGGGG	659
XX	regulatory element (TSRE), and a TAF binding site (TBS), and a second	QY	708	GGCAGCTCTCAGACGATGAGGCGAGTCTGAGGCTGAAAGAGGAGGAGGCTCGA	767
XX	expression cassette comprising a second coding region that encodes a	DB	660	GGCAGCTCTCAGACGATGAGGCGAGTCTGAGGCTGAAAGAGGAGGAGGCTCGA	719
XX	selected polypeptide, the second coding region being positioned under the	QY	768	GCCCAGGCTCTCAGACGCTCTCAGAGCTGAAAGAGGAGGAGGAGGCTCTCAGAGG	827
XX	transcriptional control of a second promoter comprising a TSRE and a TBS,	DB	720	GCCCAGGCTCTCAGAGCTCTCAGAGCTGAAAGAGGAGGAGGAGGCTCTCAGAGG	779
XX	or a TBS. The expression vector further comprises a third coding region	QY	828	CCTCAGCAGGAGGAGGCTGCGCTTACCCACAGGAGGAGGAGGCTCTCAGAGGCTCGG	887
XX	that encodes a first transcriptional silencer (TSI), the third coding	DB	780	CCTCAGCAGGAGGAGGCTGCGCTTACCCACAGGAGGAGGAGGCTCTCAGAGGCTCGG	839
XX	region being positioned under the transcriptional control, a third	QY	888	CTCCGCTCCTAGGAGGAGGCTGCGCTTACCCACAGGAGGAGGAGGCTCTCAGAGGCTCGG	947
XX	promoter comprising a TSRE and a TAB, and a fourth expression cassette	DB	840	CTCCGCTCCTAGGAGGAGGCTGCGCTTACCCACAGGAGGAGGAGGCTCTCAGAGGCTCGG	899
XX	comprising a fourth coding region that encodes a second TSI, the fourth	QY	948	AGAAAGCAACAGGAAACCCATGCTGAAATCTAGGATTTTCAAAACAAGG	1001
XX	coding region being positioned under the transcriptional control of a	DB	900	AGAAAGCAACAGGAAACCCATGCTGAAATCTAGGATTTTCAAAACAAGG	953
XX	fourth promoter that is negatively regulated by the first TSI, where the	XX	RESULT 9		
XX	first, second and third promoters are negatively regulated by the second	XX	ADV23865		
XX	TSI. The selected polypeptide is a therapeutic polypeptide, such as an	XX	ID	ADV23865	standard; DNA; 4293 BP.
XX	anti-cancer polypeptide that is a tumor suppressor, and inducer of	XX	AC	ADV23865;	
XX	apoptosis, and cell cycle regulator, a toxin, or an inhibitor of	XX	DT	24-FEB-2005	(first entry)
XX	angiogenesis, and an enzyme, a cytokine, a hormone, a tumor antigen, a	XX	XX		
XX	human antigen or a pathogen antigen. The selected polypeptide is				
XX	essential for vector replication, where the vector is an adenoviral				
XX	vector. The expression vector is useful in methods for treating cancer				
XX	and further comprises a selectable or screenable marker. The methods and				
XX	compositions of the present invention are useful in the fields of				
XX	molecular biology and gene therapy, particularly to the combined spatial				
XX	and quantitative regulation of transgene expression in eukaryotic cells,				
XX	and in treating cancer including breast cancer, ovarian cancer, fallopian				
XX	tube cancer, cervical cancer, uterine cancer, prostate cancer, testicular				
XX	cancer, pancreatic cancer, colon cancer, bladder cancer, liver cancer,				
XX	stomach cancer, lung cancer, lymphoid cancer, brain cancer, thyroid				
XX	cancer, head and neck cancer, skin cancer or leukemia. The cancer is a				
XX	recurrent cancer, a metastatic cancer or a drug resistant cancer. The				
XX	methods and compositions can also be used in treating cystic fibrosis,				
XX	AIDS, sickle cell anemia, hemophilia, diabetes, heart disease, asthma				
XX	and retinosis. The present sequence represents a human telomerase				
XX	reverse transcriptase (hTERT) gene nucleotide sequence, the promoter				
XX	fragment can be used in the vectors of the invention.				
XX	Sequence 4356 BP; 829 A; 1298 C; 1254 G; 975 T; 0 U; 0 Other;				
XX	Query Match 93.9%; Score 940.4; DB 13; Length 4356;				
XX	Best Local Similarity 99.8%; Pred. No. 2.7e-271;				
XX	Matches 952; Conservative 0; Mismatches 1; Indels 1; Gaps 1;				



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QY 314 AAGAAATTTACCCCATCGCAGGGAGTGGTTTGGGGGTTAAGACAGCGTGGGGGAGCAGC 373
DB 241 AAGATTTTACCCCATCGCAGGGAGTGGTT-GGGGGTTAAGACAGCGTGGGGGAGCAGC 299
QY 374 TGGGGGCTACTGCAAGCAGCACTTTTAAAGCCAGTTTCCTGGTTCTGTGATGTTGGCT 433
DB 300 TGGGGGCTACTGCAAGCAGCACTTTTAAAGCCAGTTTCCTGGTTCTGTGATGTTGGCT 359
QY 434 CAGTTATGGAGACTTAACCATAGGGGAGTGGGAGTGGGGAGTGGGGAGTGGCCATC 493
DB 360 CAGTTATGGAGACTTAACCATAGGGGAGTGGGAGTGGGGAGTGGGGAGTGGCCATC 419
QY 494 TTTGCCATGCCGAGTGTCTGGGCAGGATAATCTCTAGAGATGCCACGCTCTGATTC 553
DB 420 TTTGCCATGCCGAGTGTCTGGGCAGGATAATCTCTAGAGATGCCACGCTCTGATTC 479
QY 554 CCCCAAACTGTGTGACAGAAACCCCGCCGCGCCAGGGCCTTTGAGGTGTGATCTCCGTG 613
DB 480 CCCCAAACTGTGTGACAGAAACCCCGCCGCGCCAGGGCCTTTGAGGTGTGATCTCCGTG 539
QY 614 AGAACCTTGAGTCTGGATCTTTCGGACTACCTGACGGCCCGAAAGTAATCCAGGG 673
DB 540 AGAACCTTGAGTCTGGATCTTTCGGACTACCTGACGGCCCGAAAGTAATCCAGGG 599
QY 674 TTTCTGGGAAGAGCGCGCAGGAGGTCTAGAGGGGGGAGCCCTCAGGACGATGGAGGCA 733
DB 600 TTTCTGGGAAGAGCGCGCAGGAGGTCTAGAGGGGGGAGCCCTCAGGACGATGGAGGCA 659
QY 734 CAGTCTGAGGCTGAAAAGGGAGGGAGGCGCTCGAGCCCGAGCCCTGCAAGCGCTCCAGAA 793
DB 660 CAGTCTGAGGCTGAAAAGGGAGGGAGGCGCTCGAGCCCGAGCCCTGCAAGCGCTCCAGAA 719
QY 794 GCTGGAAAAGCGGGGAAGGAGACCTTCAAGAGCTGTCAGCAGAGAGGACGAGCTGGCC 853
DB 720 GCTGGAAAAGCGGGGAAGGAGACCTTCAAGAGCTGTCAGCAGAGAGGACGAGCTGGCC 779
QY 854 CTTAGCCCAACAGGGCCCATCGTGACCTCGGCGCTCGTGCCATAGGAGGCACTCGCG 913
DB 780 CTTAGCCCAACAGGGCCCATCGTGACCTCGGCGCTCGTGCCATAGGAGGCACTCGCG 839
QY 914 CTGCGCTTCTAGCATGAAGTGTGGGGATTTGAGAGCAACAGGAAACCCATGCACTG 973
DB 840 CTGCGCTTCTAGCATGAAGTGTGGGGATTTGAGAGCAACAGGAAACCCATGCACTG 899
QY 974 TGAATCTAGGATTAATTCAAAACAAAG 1001
DB 900 TGAATCTAGGATTAATTCAAAACAAAG 927
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## RESULT 10

AAH41091  
ID AAH41091 standard; DNA; 3962 BP.

AC AAH41091;

DT 29-AUG-2001 (first entry)

DE Telomerase reverse transcriptase (TERT) DNA.

KW Phenotype switch molecule; phenotype-related gene battery;  
KW gene localisation; telomere reverse transcriptase; TERT; ds.

OS Unidentified.

PN WO200138515-A1.

XX 31-MAY-2001.

XX 17-NOV-2000; 2000WO-CN000427.

XX 19-NOV-1999; 99CN-00121466.

(BIAN/) BIAN X.

Bian X;

WPI; 2001-367684/38.

Isolating phenotype switch molecules and phenotype-related gene batteries from complex genomes of higher animals and plants, useful e.g. in gene localization and classification analysis.

Example 7; Page 27-29; 35pp; Chinese.

This invention relates to a method for isolating phenotype switch molecules and phenotype-related gene batteries from complex genomes of higher animals and plants. The method is useful in gene localisation and classification analysis, studying gene development networks and function networks, and designing drugs based on regulatory sequences of the phenotypes for disease treatment. The present sequence represents DNA encoding a telomere reverse transcriptase (TERT), which is used in an example illustrating the use of the method of the invention

Sequence 3962 BP; 782 A; 1157 C; 1113 G; 910 T; 0 U; 0 Other;

Query Match 86.9%; Score 869.4; DB 4; Length 3962;

Best Local Similarity 99.8%; Pred. No. 5.5e-250;

Matches 881; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 119 GCTACAAGCAGGGAAATCCCTGCTAAATGTCTTTAAACAACCTGTTAAACAACACGG 178
DB 1 GCTACAAGCAGGGAAATCCCTGCTAAATGTCTTTAAACAACCTGTTAAACAACACGG 60
QY 179 TCCATCCGACGGTGGACAGTTCTCAGGTGAAGAGAAACATCCCGTTTATAAGCCTG 238
DB 61 TCCATCCGACGGTGGACAGTTCTCAGGTGAAGAGAAACATCCCGTTTATAAGCCTG 120
QY 239 CAGGCATCTCAAGGGAATTACGTGAGTCAAACTGCCACTCTCATGGGATACGTACGCA 298
DB 121 CAGGCATCTCAAGGGAATTACGTGAGTCAAACTGCCACTCTCATGGGATACGTACGCA 180
QY 299 ACATGCTCAAAAAGAAAGATTTTCAACCCATGGCAGGGAGTGGTTGGGGGTTAAGGAC 358
DB 181 ACATGCTCAAAAAGAAAGATTTTCAACCCATGGCAGGGAGTGGTT-GGGGGTTAAGGAC 239
QY 359 GGTGGGGGACAGCAGCTGGGGGCTACTGCACGACCTTTTACTAAAGCCAGTTTCTCGTT 418
DB 240 GGTGGGGGACAGCAGCTGGGGGCTACTGCACGACCTTTTACTAAAGCCAGTTTCTCGTT 299
QY 419 CTGATGGTATTGGCTCAGTTTATGGGAGACTAACCATAGGGAGTGGGATGGGGAAACCC 478
DB 300 CTGATGGTATTGGCTCAGTTTATGGGAGACTAACCATAGGGAGTGGGATGGGGAAACCC 359
QY 479 GGAGGCTGTGCCATCTTTGCCATGCCGAGTGTCTTGGGAGGATTAATGCTTAGAGATG 538
DB 360 GGAGGCTGTGCCATCTTTGCCATGCCGAGTGTCTTGGGAGGATTAATGCTTAGAGATG 419
QY 539 CCCAGCTCTGATTCCTCCCAAACTGTGGACAGAAACCCCGCCCGCCAGAGCCCTTTGCA 598
DB 420 CCCAGCTCTGATTCCTCCCAAACTGTGGACAGAAACCCCGCCCGCCAGAGCCCTTTGCA 479
QY 599 GGTGTGATCTCCGTGAGGACCTTGAAGTCTGGGATCTCTTGGGACTACTTGCAGGCCCGA 658
DB 480 GGTGTGATCTCCGTGAGGACCTTGAAGTCTGGGATCTCTTGGGACTACTTGCAGGCCCGA 539
QY 659 AAAGTAATCCAGGGGTTCTGGGAAGAGCGGGCAGGAGGTCAGAGGGGGGAGCCTCAG 718
DB 540 AAAGTAATCCAGGGGTTCTGGGAAGAGCGGGCAGGAGGTCAGAGGGGGGAGCCTCAG 599
QY 719 GACGATGAGGAGCAGTCAAGTCTGAGGCTGAAAAGGAGGAGGAGGCTCTGAGCCAGGCTG 778
DB 600 GACGATGAGGAGCAGTCAAGTCTGAGGCTGAAAAGGAGGAGGAGGCTCTGAGCCAGGCTG 659
QY 779 CAAGCGCTCCAGAAAGCTGGGAAAAGCGGGGAAGGGAACCTTCCACGAGCCTGCAAGAGG 838
```

Db 660 CAAGCGCTCCAGAGCTGGAAGGCGGGGAGAGGACCCCTCCACGAGCGCTCGACGAG 719  
Qy 839 AAGCGAGGCTGCGCTTACCGACACGAGGCGCCATCGTGACCTCCGGCTCCGTGCGCAT 898  
Db 720 AAGCGAGGCTGCGCTTACCGACACGAGGCGCCATCGTGACCTCCGGCTCCGTGCGCAT 779  
Qy 899 AGGAGGCGCACTCGCGCTGCGCTTCTAGCATGAAGTGTCGGGATTTGCAGAGCAACAG 958  
Db 780 AGGAGGCGCACTCGCGCTGCGCTTCTAGCATGAAGTGTCGGGATTTGCAGAGCAACAG 839  
Qy 959 GAAACCCATGCACTGGAATCTAGGATTTATTTCAAAACAAGG 1001  
Db 840 GAAACCCATGCACTGGAATCTAGGATTTATTTCAAAACAAGG 882

RESULT 11

ABL92334  
ID ABL92334 standard; DNA; 4356 BP.

AC ABL92334;

XX 01-JUL-2002 (first entry)

XX Chemically treated DNA repair gene fragment#72.

XX DNA repair; cytosine methylation; PMS2L1; PMS2L12; PMS2L3; PMS2;  
KW L4; PMS2L5; PMS2L6; MGMT; MSH2; NUDT1; TDG; INPPL1; RFC4; DDITL; FANCB;  
KW XRCCB; ataxia telangiectasia; aging; Bloom's syndrome; Cockayne syndrome;  
KW Nijmegen breakage syndrome; Werner syndrome; immunodeficiency;  
KW trichothiodystrophy; Fanconi's anaemia; solid tumour; cancer; ds.  
XX Unidentified.

XX WO200181622-A2.

XX 01-NOV-2001.

XX 06-APR-2001; 2001WO-EP003972.

XX 06-APR-2000; 2000DE-01019058.

PR 07-APR-2000; 2000DE-01019173.

PR 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

PI WPI; 2002-034446/04.

XX New nucleic acid derived from genes associated with DNA repair, useful  
PT for diagnosis, e.g. of ataxia telangiectasia, by determination of  
PT cytosine methylation.

XX Claim 1; SEQ ID NO 143; 25pp + Sequence Listing; English.

XX The invention relates to nucleic acids containing a sequence of at least  
CC 18 nucleotides of chemically treated DNA of genes associated with DNA  
CC repair, and their complements. The invention also relates to nucleic  
CC acids comprising at least 18 base pairs of the chemically pretreated DNA  
CC of genes associated with DNA repair selected from PMS2L1, PMS2L12,  
CC PMS2L2, PMS2L3, PMS2, L4, PMS2L5, PMS2L6, MGMT, MSH2, NUDT1, TDG, INPPL1,  
CC RFC4, DDITL, FANCB, or XRCCB. Nucleic acids of the invention and related  
CC oligomers, are useful for diagnosis of diseases associated with gene  
CC repair, specifically ataxia telangiectasia, aging, Bloom's syndrome,  
CC Cockayne syndrome, Nijmegen breakage syndrome or Werner syndrome,  
CC immunodeficiency, trichothiodystrophy, Fanconi's anaemia, solid tumours  
CC and/or by detecting single-nucleotide polymorphisms. Determination of  
CC individual methylation patterns may allow development of individualised  
CC therapies. The sequences given in records ABL92192-ABL92335 represent  
CC chemically pre-treated DNA fragments from genes associated with DNA  
CC repair, and their complements. Note: The sequence data for this patent is

CC not represented in the specification, but is based on sequence  
CC information supplied by the European Patent Office  
XX  
SQ Sequence 4356 BP; 829 A; 218 C; 1254 G; 2055 T; 0 U; 0 Other;  
Query Match 59.7%; Score 598; DB 6; Length 4356;  
Best Local Similarity 77.4%; Pred. No. 2e-168;  
Matches 738; Conservative 0; Mismatches 215; Indels 1; Gaps 1;  
Qy 48 GAATTCACGTGACCTACGCACATCATGTACACATCTCCCGTCCACGACGACCCCGCTGTT 107  
Db 1 GAATTTACGTGATTACGTATATATGTATATATTTTCGTTACGATCGATTTTCGTTGTT 60  
Qy 108 TTATTTTAAATAGCTACAAAGCAGGGAATCCCTGCTAAATATGTCCTTTAAACAACCTGTT 167  
Db 61 TTATTTTAAATAGTTATAAAGTAGGGAATTTTGTGTTAAATGTTTTTAAATTAATTTGTT 120  
Qy 168 AAACAAACGGGTCCATCCGACGTCGACAGATTCCTCACAGTGAAGAGGAACAATGCCGTT 227  
Db 121 AAATAAACGGGTTTATTCGTACGCTGGATAGTTTTTTTATAGTGAAGAGGATATGCTTT 180  
Qy 228 TATAAAGCCTGCAGGCATCTCAAGGGAATTTACGCTGAGTCAAAACTGCCACCTCCATGGG 287  
Db 181 TATAAAGTTTGTAGGTATTTTAAGGGAATTTACGTTGAGTTAAATTTGTTATTTTATGGG 240  
Qy 288 ATACGTACGCACATCTCAAAAGAAAGAAATTTTACCCCATGGCAGGGAGTGGTGGG 347  
Db 241 ATACGTACGTAAATATTTTAAAGAAAGAAATTTTATTTATGTTAGGGAGTGGTT-GG 299  
Qy 348 GGGTTAAGGACCGTGGGGGCGAGCAGCTGGGGGCTACTGCACGACACCTTTTACTAAAGCCA 407  
Db 300 GGGTTAAGGACCGTGGGGGCTAGTTGGGGTTATTTGACGTATTTTATTATTAAGTTA 359  
Qy 408 GTTTCCTGTTCTGATGTATTTGGCTCAGTTATGGAGACTAACCATAGGGAGTGGGA 467  
Db 360 GTTTTTCGTTTTGATGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 419  
Qy 468 TGGGGGAACCGGGAGCTGTGCCATCTTTGCCATGCCGAGTGTCTTGGGACGATTAATG 527  
Db 420 TGGGGGAATTCGGAGGTTGTGTTATTTTGTATGTTTCGAGTGTTTGGGTAGGATAATG 479  
Qy 528 CTCTAGAGATGCCACGCTCTGATTCCTCCCAACCTGTGCACAGAACCCCGCCGCCCA 587  
Db 480 TTTTAGAGATGTTACGTTTGAATTTTAAATTTTGGATAGATTCGTTGCTGTTTAA 539  
Qy 588 GGGCTTTTGACGGTGTGATCTCGTGAGACCTCGTGGAGTCTGGGATCTCTTCCGGAATACC 647  
Db 540 GGGTTTTTCGTAGGTGTGATTTTCGTGAGGATTTTGGAGTTTGGGATTTTTCGGGATATT 599  
Qy 648 TGCAGGCCCGAAAGTAATCCAGGGGTTCTGGGAGAGGGGGCGAGGGGTCCAGAGGGG 707  
Db 600 TGTAGGTTTGAAAAGTAATTTAGGGGTTTGGGAGAGGGCGGTAGAGGGTTAGAGGGG 659  
Qy 708 GGCAGCCTCAGGACGATGGAGGCGAGTCAGTCTGAGGCTGAAAAGGAGGAGGGGCTCGA 767  
Db 660 GGTAGTTTTCGACGATGGAGGTAGTTAGTTGAGGTTGAAAAGGAGGAGGGGTTTGA 719  
Qy 768 GCCAGGCTGCAAGCGCTCCAGAGAGCTGGAAGGAGGAGGAGGAGCCCTCCAGGAG 827  
Db 720 GTTTAGGTTTGAAGCGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTT 779  
Qy 828 CTGTCAGCAGGAGGACGCGCTGGCCCTTAGCCCAACAGGGCCCATCGTGACCTCCGGC 887  
Db 780 TTTGTAGTAGGAGGTACCGTTGTTTTTGTAGTTTATTTAGGGTTTTCGTGATTTTCGGT 839  
Qy 888 CTCCTGTCATAGGAGGCGACCTCGCGCTGCTCCCTCTTAGCATGAAGTGTGTGGGATTTGC 947  
Db 840 TTTTCGTTTATAGGAGGTATTCGCTGTTGTTTTTTTATGATGAAGTGTGTGGGATTTGT 899  
Qy 948 AGAAGCAACAGGAAACCCATGCACTGTGAATCTAGGATTTATTTCAAAACAAGG 1001  
Db 900 AGAAGTAATAGGAAATTTATGTTATTTAGGATTTAGGATTTATTTTAAATAAAGG 953

RESULT 12	Db	4295	TAATTTAAATACAACTACAAACAAATAATCCCTACTAAATATCTCTTAAACAACTAATTA	4236
ABL92335/c	Qy	169	AACAAACGGGTCCATCCGACGGTGGACAGTTCCTCACAGTGAAGAGGAAACATCCCGTTT	228
ID ABL92335 standard; DNA; 4356 BP.	Db	4235	AACAAACGAATCCATCCGACGATAAACAATTCCTCAATATAAATAAACAATACCGTTT	4176
AC ABL92335;	Qy	229	ATAAAGCCTCAGGCATCTCAAGGGAAATTACGTGAGTCAAAACTGCCACCTCCATGGGA	288
XX 01-JUL-2002 (first entry)	Db	4175	ATAAACCTACAAACATCTCAAAAAAATTAGCTAAATCAAACTACACCTCCATAAAA	4116
XX Chemically treated DNA repair gene fragment complementary to #72.	Qy	289	TACGTAGCAACATGCTCAAAAAGAAAGATTTTACCCCATGGCAGGGAGTGTGGGG	348
XX DNA repair; cytosine methylation; PMS2L1; PMS2L12; PMS2L3; PMS2;	Db	4115	TACGTAGCAACATGCTCAAAAAGAAAGATTTTACCCCATGGCAGGGAGTGTGGGG	4057
XX L4; PMS2L5; PMS2L6; MGMT; MSH2; NUDT1; TDG; INPPL1; RFC4; DDITL1; FANCB;	Qy	349	GGTTAAGGAGCGTGGGGGACGAGCTGGGGGCTACTGCAGCAGCTTTTACTAAGCCAG	408
XX XRC8; ataxia telangiectasia; aging; Bloom's syndrome; Cockayne syndrome;	Db	4056	AAATTAATAAACGATAAAAAACAACTAAATACTACTACGACCTTTTCTATAAACCA	3997
XX Nijmegen breakage syndrome; Werner syndrome; immunodeficiency;	Qy	409	TTTCTCTGTTCTGATGTTATTTGGCTCAGTTATGGGAGACTAAACATAGGGAGTGGGAT	468
XX trichiodystrophy; Fanconi's anaemia; solid tumour; cancer; ds.	Db	3996	TTTCTCTGTTCTGATGTTATTTGGCTCAGTTATGGGAGACTAAACATAGGGAGTGGGAT	3937
XX Unidentified.	Qy	469	GGGGAAACCCGGAGGTGTGCTATTTTGGCATGCCGAGTGTCTTGGGAGGAGTAATGC	528
XX OS WO200181622-A2.	Db	3936	AAAAAAACCCGAAACATATACCATCTTTACCATACCCGAAATATCTTAAACAAAATAAT	3877
XX PN WO200181622-A2.	Qy	529	TCTAGATGCCACGCTCTGATTTCCGCCAACCCTGTGGACAGACCGCCGCCGCCAG	588
XX PD 01-NOV-2001.	Db	3876	TCTAAAAATACCCACGCTCTTAAATTTCCCCCAACCTATAAACAACACCCGCCGCCCA	3817
XX PF 06-APR-2001; 2001WO-EP003972.	Qy	589	GGCCTTTGCGAGGTGTGATCTCCGTCGAGGACCTCTGAGGTCTGGGATCTTCCGGGACTACT	648
XX PR 06-APR-2000; 2000DE-01019058.	Db	3816	AACCTTTTACAATATATATCTCCGTAAAAACCTTAAATCTTAAATCTTCCAACTACT	3757
XX PR 07-APR-2000; 2000DE-01019173.	Qy	649	GCAGGCCCGAAAAAGTAAATCCAGGGGTTCTGGGAAAGAGCGGGCAGGAGGTCCAGAGGGG	708
XX PR 30-JUN-2000; 2000DE-01032529.	Db	3756	ACAAACCCGAAAAATAATCCAAAAATTTCTAAAAAACAACGAAACAAAAAATCAAAAAA	3697
XX PR 01-SEP-2000; 2000DE-01043826.	Qy	709	GCAGCTTCAGGACGATGGAGGCGCTCAGTCTGAGGCTGAAAGGAGGAGGGGCTCGAG	768
XX PA (EPIG-) EPIGENOMICS AG.	Db	3696	ACAACTCAAAACGATAAAAACCAATCAATCTTAAACCTAAAAAATAAATAAATAAATAA	3637
XX PI Olek A, Piepenbrock C, Berlin K;	Qy	769	CCAGGCTCTCAGCGCTCCAGAGCTCCAGAAAGCGGGAAGGAGGAGCCCTCCACGGAGC	828
XX PL WPI; 2002-034446/04.	Db	3636	CCCAAACTCAAAACGCTCCAAAACTTAAAAAATAAATAAATAAATAAATAAATAAATAA	3577
XX PR New nucleic acid derived from genes associated with DNA repair, useful	Qy	829	CTGACAGGAGGACGAGTGGGCTTACGCCACACGAGGCGCCATCGTGGACCTCCGGCC	888
XX PT for diagnosis, e.g. of ataxia telangiectasia, by determination of	Db	3576	CTACAAACAAAAAACAGACTAACCCCTTAAACCCCAAAACCCATCGTAAACCTCCGACC	3517
XX PT cytosine methylation.	Qy	889	TCCGTGCTATAGGAGGACCTCCGGCTCCGCTTCTAGCATGAAGTGTGGGATTTGCA	948
XX PS Claim 1; SEQ ID NO 144; 25pp + Sequence Listing; English.	Db	3516	TCCGTACCTAAAAAACAACCTCCGCTTCTTAACTAAATAAATAAATAAATAAATAAATAA	3457
XX CC The invention relates to nucleic acids containing a sequence of at least	Qy	949	GAACCAACAGAAACCCATGCATCTGCAATCTAGGATTTTCAAAACAAA	999
XX CC 18 nucleotides of chemically treated DNA of genes associated with DNA	Db	3456	AAAAACAAACAAAAACCCATACACTATTAATTAATTAATTAATTAATTAATTAATTAAT	3406
XX CC repair, and their complements. The invention also relates to nucleic	RESULT 13			
XX CC acids comprising at least 18 base pairs of the chemically pretreated DNA	ABL9235670			
XX CC of genes associated with DNA repair selected from PMS2L1, PMS2L12,	ID ABL9235670 standard; DNA; 480 BP.			
XX CC PMS2L2, PMS2L3, PMS2L4, PMS2L5, MGMT, MSH2, NUDT1, TDG, INPPL1,	XX AC ABL9235670;			
XX CC RFC4, DDITL1, FANCB, or XRC8. Nucleic acids of the invention and related	XX AC ABL9235670;			
XX CC oligomers, are useful for diagnosis of diseases associated with gene	DT 15-MAY-2003 (first entry)			
XX CC repair, specifically ataxia telangiectasia, aging, Bloom's syndrome,	XX AC ABL9235670;			
XX CC Cockayne syndrome, Nijmegen breakage syndrome or Werner syndrome,	DE Human TERT promoter region.			
XX CC immunodeficiency, trichiodystrophy, Fanconi's anaemia, solid tumours	XX HLTF; carcinogenesis; hyperproliferative lesion; cytostatic; virucide;			
XX CC and cancer, particularly by determining status of cytosine methylation	XX helicase-like transcription factor; telomerase reverse transcriptase;			
XX CC and/or by detecting single-nucleotide polymorphisms. Determination of	XX dermatological; gynaecological; TERT; gene therapy; cancer; human; ds.			
XX CC individual methylation patterns may allow development of individualised				
XX CC therapies. The sequences given in records ABL92192-ABL92335 represent				
XX CC chemically pre-treated DNA fragments from genes associated with DNA				
XX CC repair, and their complements. Note: The sequence data for this patent is				
XX CC not represented in the specification, but is based on sequence				
XX CC information supplied by the European Patent Office				
XX SQ Sequence 4356 BP; 975 A; 218 C; 1298 G; 1865 T; 0 U; 0 Other;				
XX Query Match 53.5%; Score 535.8; DB 6; Length 4356;				
XX Best Local Similarity 73.4%; Pred. No. 9.9e-150;				
XX Matches 698; Conservative 0; Mismatches 253; Indels 1; Gaps 1;				
Qy 49 AATTCAGTGTAGGACATCATGTACACTCCGTCGACGAGCGACCGCCCGCTGTTT	108			
Db 4355 AATTCAGTGTAGGACATCATGTACACTCCGTCGACGAGCGACCGCCCGCTGTTT	4296			
Qy 109 TATTTTATAGTACAAAGCAGGGAATCCCTGCTTAAATATGCTTTTAAACAACTGGTTA	168			

XX OS	Homo sapiens.	Db	420	TGGGGGACCCGAGGCTGTGCCATCTTTGCCATGCCGAGTCTCTGGGAGGATATG	479
XX FN	WO2003002068-A2.	Qy	528	C 528	
XX PD	09-JAN-2003.	Db	480	C 480	
XX PF	27-JUN-2002; 2002WO-US020757.				
XX PR	27-JUN-2001; 2001US-0301384P.				
XX PA	(NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.				
XX PI	Androphy EJ, Doshi N, Delayew A;				
XX DR	WPI; 2003-210197/20.				
XX PT	Inhibiting carcinogenesis of a cell, especially useful for treating a				
XX PT	human papilloma virus-mediated hyperproliferative lesion (warts) or				
XX PT	cancer, by reducing the activity of helicase-like transcription factor in				
XX PT	the cell.				
XX PS	Claim 18; Fig 6; 36pp; English.				
XX CC	The invention relates to inhibiting carcinogenesis of a cell, or				
XX CC	inhibiting growth of a cell in a human papillomavirus (HPV)-mediated				
XX CC	hyperproliferative lesion. The method involves reducing the amount of				
XX CC	helicase-like transcription factor (HLTF) in the cell or inhibiting the				
XX CC	binding of endogenous HLTF to telomerase reverse transcriptase (TERT)				
XX CC	promoter. The method is useful for inhibiting carcinogenesis of a cell,				
XX CC	or inhibiting growth of a cell in an HPV-mediated hyperproliferative				
XX CC	lesion. The method is particularly useful for treating cancer (especially				
XX CC	cervical cancer), or hyperproliferative lesions (warts) caused by HPV.				
XX CC	The method is also useful for diagnosing a neoplasm, or detecting the				
XX CC	presence of a malignant tumour or a predisposition to developing the				
XX CC	tumour. The present sequence represents the hTERT promoter region to				
XX CC	which HLTF binds to				
XX SQ	Sequence 480 BP; 125 A; 117 C; 131 G; 107 T; 0 U; 0 Other;				
	Query Match 46.7%; Score 467.4; DB 8; Length 480;				
	Best Local Similarity 99.6%; Pred. No. 1.3e-129;				
	Matches 479; Conservative 0; Mismatches 1; Indels 1; Gaps 1;				
Qy	48 GAATTCACGCTACGACATCATGTACACATCCCGTCCAGCAGCCGCGCTGTT	107			
Db	1 GAATTCACGCTACGACATCATGTACACATCCCGTCCAGCAGCCGCGCTGTT	60			
Qy	108 TTATTTTAATAGCTACAAAGCAGGGAATCCCTGCTAAATGTCCTTAAACAACTGGTT	167			
Db	61 TTATTTTAATAGCTACAAAGCAGGGAATCCCTGCTAAATGTCCTTAAACAACTGGTT	120			
Qy	168 AAACAAACGGGTCCATCCGACCGGTGGACAGTTCTCTCAGAGTGAAGAGAACATGCCGTT	227			
Db	121 AAACAAACGGGTCCATCCGACCGGTGGACAGTTCTCTCAGAGTGAAGAGAACATGCCGTT	180			
Qy	228 TATAAGCCTGCAGGATCTCAAGGAAATTCGCTGATCAAACTCCACCTCCATGGG	287			
Db	181 TATAAGCCTGCAGGATCTCAAGGAAATTCGCTGATCAAACTCCACCTCCATGGG	240			
Qy	288 ATAGTGACGCAACATGCTCAAAAGAAAGAAATTTACCCCATGCGAGGAGTGGTGGG	347			
Db	241 ATAGTGACGCAACATGCTCAAAAGAAAGAAATTTACCCCATGCGAGGAGTGGTGGG	299			
Qy	348 GGGTTAAGGACGGTGGGGGAGCAGCTGGGGGCTACTGCAACGACCTTTTACTAAAGCCA	407			
Db	300 GGGTTAAGGACGGTGGGGGAGCAGCTGGGGGCTACTGCAACGACCTTTTACTAAAGCCA	359			
Qy	408 GTTTCCTGGTCTGATGGTATTGGCTCAGTTATGGGAGACTAACATAGGGAGTGGGA	467			
Db	360 GTTTCCTGGTCTGATGGTATTGGCTCAGTTATGGGAGACTAACATAGGGAGTGGGA	419			
Qy	468 TGGGGGAACCGGAGGCTGTGCCATCTTTGCCATGCCGAGTGTCTCTGGGAGGATAATG	527			

RESULT 14

ID ADU82631 standard; DNA; 5491 BP.

XX AC ADU82631;

XX DT 10-FEB-2005 (first entry)

XX DE Human hTERT gene nucleotide sequence.

XX KW Gene expression; transcription; TERT; telomerase reverse transcriptase;

XX KW cancer therapy; cytostatic; CNS; respiratory; anti-HIV; antianemic;

XX KW antischlicking; hemostatic; antidiabetic; cardiant; antiinflammatory;

XX KW antirheumatic; antiarthritic; neuroprotective; antidiabetic; vasotropic;

XX KW gene therapy; apoptosis stimulator; cancer; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 3415..3633

XX FT /tag=a

XX FT /product="telomerase reverse transcriptase fragment"

XX FT /partial

XX PN WO2004099377-A2.

XX XX 18-NOV-2004.

XX XX 30-APR-2004; 2004WO-US013487.

XX PR 01-MAY-2003; 2003US-0467171P.

XX (MUSC-) MUSC FOUND RES DEV.

XX Dong J, Rubinchik S, Woraratanadham J;

XX WPI; 2004-805118/79.

XX P-PSDB; ADU82632.

XX GENBANK; AB016767.

XX New expression vector comprising a first expression cassette with a first

XX coding region that encodes a transcriptional activating factor (TAP),

XX useful in treating cancer, AIDS, hemophilia, diabetes and asthma.

XX Disclosure; SEQ ID NO 3; 112pp; English.

XX The invention relates to an expression vector comprising a first

XX expression cassette having a first coding region that encodes a

XX transcriptional activating factor (TAP), and a second expression cassette

XX comprising a second coding region that encodes a selected polypeptide.

XX The expression vector further comprises a first expression cassette

XX having a first coding region that encodes a transcriptional activating

XX factor (TAP), the first coding region being positioned under the

XX transcriptional control of a first promoter comprising a tissue specific

XX regulatory element (TSRE), and a TAF binding site (TBS), and a second

XX expression cassette comprising a second coding region that encodes a

XX selected polypeptide, the second coding region being positioned under the

XX transcriptional control of a second promoter comprising a TSRE and a TBS,

XX or a TBS. The expression vector further comprises a third coding region

XX that encodes a first transcriptional silencer (TSI), the third coding

XX region being positioned under the transcriptional control, a third

XX promoter comprising a TSRE and a TAF, and a fourth expression cassette

XX comprising a fourth coding region that encodes a second TSI, the fourth

XX coding region being positioned under the transcriptional control of a

XX fourth promoter that is negatively regulated by the first TSI, where the

CC first, second and third promoters are negatively regulated by the second  
CC TSI. The selected polypeptide is a therapeutic polypeptide, such as an  
CC anti-cancer polypeptide that is a tumor suppressor, and inducer of  
CC apoptosis, and cell cycle regulator, a toxin, or an inhibitor of  
CC angiogenesis, and an enzyme, a cytokine, a hormone, a tumor antigen, a  
CC human antigen or a pathogen antigen. The selected polypeptide is  
CC essential for vector replication, where the vector is an adenoviral  
CC vector. The expression vector is useful in methods for treating cancer  
CC and further comprises a selectable or screenable marker. The methods and  
CC compositions of the present invention are useful in the fields of  
CC molecular biology and gene therapy, particularly to the combined spatial  
CC and quantitative regulation of transgene expression in eukaryotic cells,  
CC and in treating cancer including breast cancer, ovarian cancer, fallopian  
CC tube cancer, cervical cancer, uterine cancer, prostate cancer, testicular  
CC cancer, pancreatic cancer, colon cancer, bladder cancer, liver cancer,  
CC stomach cancer, lung cancer, lymphoid cancer, brain cancer, thyroid  
CC cancer, head and neck cancer, skin cancer or leukemia. The cancer is a  
CC recurrent cancer, a metastatic cancer or a drug resistant cancer. The  
CC methods and compositions can also be used in treating cystic fibrosis,  
CC AIDS, sickle cell anemia, hemophilia, diabetes, heart disease,  
CC inflammatory disorders, rheumatoid arthritis, multiple sclerosis, asthma  
CC and restenosis. The present gene represents a human telomerase  
CC reverse transcriptase (hTERT) gene nucleotide sequence, the promoter  
CC fragment can be used in the vectors of the invention.

SQ Sequence 5491 BP; 954 A; 1729 C; 1677 G; 1131 T; 0 U; 0 Other;

Query Match 37.1%; Score 371; DB 13; Length 5491;  
Best Local Similarity 100.0%; Pred. No. 3.6e-100;  
Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 631 GATCCTTCGGGACCTACCTGACGGCCGGAAGTAAATCCAGGGGTTCTGGGAAGGCGGG 690  
DB 1 GATCCTTCGGGACCTACCTGACGGCCGGAAGTAAATCCAGGGGTTCTGGGAAGGCGGG 60  
QY 691 CAGGAGGCTCAGAGGGGGCGGACCTCAGGACGATGGAGGCACTGAGTCTGAGGCTGAAAA 750  
DB 61 CAGGAGGCTCAGAGGGGGCGGACCTCAGGACGATGGAGGCACTGAGTCTGAGGCTGAAAA 120  
QY 751 GGGAGGAGGGCTTCGAGCCCGAGGCTGCAAGCGCTCCAGAGCTGGAAGGCGGGGA 810  
DB 121 GGGAGGAGGGCTTCGAGCCCGAGGCTGCAAGCGCTCCAGAGCTGGAAGGCGGGGA 180  
QY 811 AGGACCTCCAGGAGCTCAGCAGAGGAGGCGGCTGAGGCTGAGCCCTAGCCACAGGGCC 870  
DB 181 AGGACCTCCAGGAGCTCAGCAGAGGAGGCGGCTGAGGCTGAGCCCTAGCCACAGGGCC 240  
QY 871 CATCGTGACCTCCGGCTCCGTCATAGAGGCGCACTCGCGCTGCGCTCTAGCATGA 930  
DB 241 CATCGTGACCTCCGGCTCCGTCATAGAGGCGCACTCGCGCTGCGCTCTAGCATGA 300  
QY 931 AGTGTGTGGGATTGCAAGAGCAACAGGAACCCATGCACTGTGAATCTAGGATTATTT 990  
DB 301 AGTGTGTGGGATTGCAAGAGCAACAGGAACCCATGCACTGTGAATCTAGGATTATTT 360  
QY 991 CAACAACAAGG 1001  
DB 361 CAACAACAAGG 371

RESULT 15  
AAA41829  
ID AAA41829 standard; cDNA; 467 BP.  
XX  
XX AAA41829;  
AC  
XX  
DT 21-AUG-2000 (first entry)  
XX  
XX Human secreted expressed sequence tag SEQ ID NO:569.  
DE  
XX Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST;  
XX expressed sequence tag; EST; probe; chemotactic; proliferative;  
KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;

KW thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;  
KW antiviral; antidiabetic; antiasthmatic; vulnary; antiparkinsonian;  
KW antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic;  
KW cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine;  
KW autoimmune disorder; multiple sclerosis; allergic condition;  
KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;  
KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;  
KW central nervous system disorder; Alzheimer's disease; stroke;  
KW Parkinson's disease; Huntington's disease; coagulation disorder;  
KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour;  
KW infection; depression; psoriasis; ss.

OS Homo sapiens.  
XX WO200021990-A1.

XX 20-APR-2000.

XX 15-OCT-1999; 99WO-US024205.

XX 15-OCT-1998; 98US-0104435P.

XX (GBMY ) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
XX Merberg D, Treacy M;

XX WPI; 2000-317937/27.

Isolated polynucleotides, and encoded proteins, comprising secreted  
expressed sequence tags (sESTs), useful for treating various disorders  
such as autoimmune, infectious, and central nervous system disorders.

Claim 1; Page 290; 618pp; English.

AAA41261 to AAA43419 represent specifically claimed secreted expressed  
sequence tags (sESTs), isolated from human, mouse, xenopus and rat tissue  
sources. The sESTs can have a range of activities depending on the  
tissues they were isolated from. The activities include: chemoractic;  
proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic;  
haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial;  
antifungal; antiviral; antidiabetic; antiasthmatic; vulnary; antilulcer;  
osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic;  
cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be  
used for gene therapy and in vaccines. The sESTs are useful as probes for  
the identification and isolation of full-length cDNAs and genomic DNA  
molecules which correspond to the sESTs. Proteins encoded by the sESTs  
are useful in assays for determining biological activity and raising  
antibodies. They may be useful for treatment of autoimmune disorders  
(multiple sclerosis, insulin dependent diabetes), allergic conditions  
(asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,  
osteoporosis, osteoarthritis, central nervous system disorders  
(Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation  
disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's  
disease), tumours, bacterial, fungal or viral infections, depression and  
psoriasis. AAA43420 to AAA43425 represent linker variants which are given  
in the exemplification of the present invention

Sequence 467 BP; 134 A; 96 C; 134 G; 103 T; 0 U; 0 Other;

Query Match 5.8%; Score 57.6; DB 3; Length 467;  
Best Local Similarity 61.7%; Pred. No. 1.7e-06;  
Matches 142; Conservative 0; Mismatches 84; Indels 4; Gaps 3;  
QY 587 AGGGCCTTTGACGGTGTGATCTCCGTGAGGACCTGAGGCTGCG-GATCCTTCGGGACTA 645  
DB 221 AGGGACITTCAGGGGTGACTGAGTAAAGATCCTCAGATGAGGAGGTTTTCATGGATTG 280  
QY 646 CCTGAGGCCCGAAAAAGTAATCCAGGGGTTCTGGGAAGAGCGGCGCAGAGGTCAGAGG 705  
DB 281 TTTGGTGGGGCCCAATGTATTCAGGATCCTTTTCAAGCAAGCAAGCAGAGGCGCAGAGT 340  
QY 706 GGGGCGGCT--CAGGACGATGGAGGCGAGTCAGTCTGAGGCTGAAAAAGGAGGAGGCC 763

Db	341	CAGAGAAACAGACACGACAAATGGAAGCAGAGGTTGGGCTGATACTGGAGTGGAGGGGCC	400
Qy	764	TCGAGCCCGCCCTGCGAGC-GCCTCCAGAGCTTGGNAAAAGCGGGGAAG	812
Db	401	ACCAGCCCAAGGAATGCGAGGCAGGCTCTAGGAGCTGGNAAAAGGCAAGAAAG	450

Search completed: January 10, 2006, 11:12:03  
Job time : 694.667 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 10:08:59 ; Search time 5387 Seconds

(without alignments)  
10562.520 Million cell updates/sec

Title: US-09-615-039-1\_COPY\_9500\_10500

Perfect score: 1001

Sequence: 1 aaagaccgcatggcac.....ggattatttcaaaacaag 1001

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: gb\_ba.\*
- 2: gb\_in.\*
- 3: gb\_env.\*
- 4: gb\_on.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_sts.\*
- 11: gb\_sy.\*
- 12: gb\_un.\*
- 13: gb\_vi.\*
- 14: gb\_btg.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1001	100.0	15332	8 AF121948	AF121948 Homo sapi
2	1001	100.0	15418	6 AR342806	AR342806 Sequence
3	1001	100.0	15418	6 AR490112	AR490112 Sequence
4	1001	100.0	15418	6 AR576878	AR576878 Sequence
5	1001	100.0	15418	6 AR453025	AR453025 Sequence
6	1001	100.0	15418	6 AX498409	AX498409 Sequence
7	1001	100.0	15418	6 AX504952	AX504952 Sequence
8	1001	100.0	92564	8 AY007685	AY007685 Homo sapi
9	1001	100.0	161252	14 AC114955	AC114955 Homo sapi
10	988.4	98.7	5126	6 AX003120	AX003120 Sequence
11	988.4	98.7	11276	6 AX003122	AX003122 Sequence
12	988.4	98.7	12213	8 AF114847	AF114847 Homo sapi
13	988.4	98.7	26414	8 HSTRT1	AF128893 Homo sapi
14	988.4	98.7	51552	6 AR266023	AR266023 Sequence
15	988.4	98.7	202305	8 AC114291	AC114291 Homo sapi
16	946	94.5	170646	14 AC123545	AC123545 Pan trogl
17	940.4	93.9	4356	8 AF097365	AF097365 Homo sapi
18	744.4	74.4	170946	14 AC117933	AC117933 Papio anu

Dowell, R.  
09/16/5039  
Seq. 101

c	19	744.4	74.4	183506	14	AC122155	AC122155 Papio anu
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c	22	371	37.1	5491	8	AB016767	AB016767 Homo sapi
c	23	62.8	6.3	250175	14	AC160494	AC160494 Bos tauru
c	24	61.2	6.1	149252	8	AC012615	AC012615 Homo sapi
c	25	60.2	6.0	175225	14	AC136941	AC136941 Homo sapi
c	26	60.2	6.0	185228	8	CNS01RGU	AL160192 Human chr
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c	28	58.8	5.9	187395	14	AC164243	AC164243 Bos tauru
c	29	58.8	5.9	260185	14	AC160299	AC160299 Bos tauru
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c	31	56.6	5.7	166287	8	AC002060	AC002060 Homo sapi
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c	40	55.4	5.5	190590	14	AC135045	AC135045 Homo sapi
c	41	55	5.5	33737	6	BD176844	BD176844 A method
c	42	55	5.5	33737	8	HSIGLAMB	XS1755 Human lambo
c	43	55	5.5	40162	8	D87017	D87017 Homo sapien
c	44	55	5.5	125020	8	AF429315	AF429315 Homo sapi
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ALIGNMENTS

RESULT 1	AF121948	AF121948	15332 bp	DNA	linear	PRI 11-APR-1999
LOCUS	AF121948	Homo sapiens telomerase reverse transcriptase (TERT) gene, partial cds.				
DEFINITION	AF121948	Homo sapiens telomerase reverse transcriptase (TERT) gene, partial cds.				
ACCESSION	AF121948	AF121948.1	GI:4580662			
VERSION	AF121948					
KEYWORDS	AF121948	Homo sapiens (human)				
SOURCE	AF121948	Homo sapiens				
ORGANISM	AF121948	Homo sapiens				
REFERENCE	AF121948	Greenberg,R.A., O'Hagan,R.C., Deng,H., Xiao,Q., Hann,S.R., Adams,R.R., Lichtsteiner,S., Chin,L., Morin,G.B. and Definho,R.A. Telomerase reverse transcriptase gene is a direct target of c-Myc but is not functionally equivalent in cellular transformation				
AUTHORS	AF121948	Greenberg,R.A., O'Hagan,R.C., Deng,H., Xiao,Q., Hann,S.R., Adams,R.R., Lichtsteiner,S., Chin,L., Morin,G.B. and Definho,R.A. Telomerase reverse transcriptase gene is a direct target of c-Myc but is not functionally equivalent in cellular transformation				
TITLE	AF121948	Oncogene 18 (5), 1219-1226 (1999)				
JOURNAL	AF121948	Oncogene 18 (5), 1219-1226 (1999)				
PUBMED	AF121948	10022128				
REFERENCE	AF121948	2 (bases 1 to 15332)				
AUTHORS	AF121948	Morin,G.B., Carlos,R. and Adams,R.R.				
TITLE	AF121948	Submitted (21-JAN-1999)				
JOURNAL	AF121948	Menlo Park, CA 94025, USA				
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promoter	AF121948	/mol_type="genomic DNA"				
mRNA	AF121948	/db_xref="taxon:9606"				
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LVAPSCAYQVQGPPLVQLGAATQAPPPHAGSPRRRLGGERAWNHVSVRBAGVPLGHPA  
PGARRGGSASRSLPLPKRPRGCAAPERTPVQGSWAHPGRTGRGSDRGFCVSPAP  
PRAEATSLGALSGLSTHSHPSVQRQHHAGFPSTSRPPRPWPDTPCPVPVATYKHFLYS  
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TWMSVRDCAWLRSP"

ORIGIN

Query Match 100.0%; Score 1001; DB 8; Length 15332;  
Best Local Similarity 100.0%; Pred. No. 9.1e-272;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAGACCCAGCATTTGGCACCCCTGGACATTTGCCACAGCCCTGGGAATTCACGCTGAC 60  
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Qy 61 TAGCGACATCATGTATACACTCCCGTCCACAGCCGACCCCGCTGTTTATTTTAAATAGC 120  
Db 9517 TAGCGACATCATGTATACACTCCCGTCCACAGCCGACCCCGCTGTTTATTTTAAATAGC 9576

Qy 121 TACAAGCAGGGAATCCCTGCTTAAATGTCTTTTAAACAACTGGTTTAAACAAACGGGTC 180  
Db 9577 TACAAGCAGGGAATCCCTGCTTAAATGTCTTTTAAACAACTGGTTTAAACAAACGGGTC 9636

Qy 181 CATCCGACCGGTGCACAGTTTCTTACAGTGAAGGAAACATCGCTTTTATAAAGCCCTGCA 240  
Db 9637 CATCCGACCGGTGCACAGTTTCTTACAGTGAAGGAAACATCGCTTTTATAAAGCCCTGCA 9696

Qy 241 GGCATCTCAAGGGAATTAACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGACCAAC 300  
Db 9697 GGCATCTCAAGGGAATTAACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGACCAAC 9756

Qy 301 ATGCTCAAAAAGAAAGAAATTTACCCCATGGCAGGAGGTGGTTGGGGGGTTAAGGACGG 360  
Db 9757 ATGCTCAAAAAGAAAGAAATTTACCCCATGGCAGGAGGTGGTTGGGGGGTTAAGGACGG 9816

Qy 361 TGGGGGACAGCTGGGGGCTACTGCACGACCTTTTACTTAAAGCCAGTTTCTCGTTCT 420  
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Db 9877 GATGGTATTGGCTCAGTTATGGGAGACTAAACATAGGGGAGTGGGATGGGGAAACCCGG 9936

Qy 481 AGGCTGTGCCATCTTTGCCATGCCCAGTGTCTTGGGACGAGTAATGCTCTAGAGATGCC 540  
Db 9937 AGGCTGTGCCATCTTTGCCATGCCCAGTGTCTTGGGACGAGTAATGCTCTAGAGATGCC 9996

Qy 541 CAGTCTCTGATTTCCCCCAACCTGTGACAGAACCCCGCCGACGAGCCCTTTCAGG 600  
Db 9997 CAGTCTCTGATTTCCCCCAACCTGTGACAGAACCCCGCCGACGAGCCCTTTCAGG 10056

Qy 601 TGTGATCTCCGTGAGGACCTCGAGTCTGGGATCTCTTGGGACTTACCTGACGGCCCGAAA 660  
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Qy 661 AGTAATCCAGGGGTTCTGGGAAGAGCGGCGAGAGGGTCAAGAGGGGCGAGCTCTCAGGA 720  
Db 10117 AGTAATCCAGGGGTTCTGGGAAGAGCGGCGAGAGGGTCAAGAGGGGCGAGCTCTCAGGA 10176

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Db 10177 CGATGGAGGACGTCACTCTGAGCTGAAGAGGAGGAGGGCTTCGAGCCAGCCCTGCA 10236

Qy 781 AGGCTCTCCAGAGCTCGAAAAAGCGGGAAGGACCTTCACGAGCCCTCGACAGCAGAA 840  
Db 10237 AGGCTCTCCAGAGCTCGAAAAAGCGGGAAGGACCTTCACGAGCCCTCGACAGCAGAA 10296

Qy 841 GSCAGGCTGGCCCTTTAGCCACAGGCGCCCATCTGGACCTCCGCGCTCCGTGCCATAG 900  
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Qy 901 GAGGCGACCTCGCGCTGCGCTTCTTAGCATGAAGTGTGTGGGGATTTGCAGAAGCAACAGGA 960  
Db 10357 GAGGCGACCTCGCGCTGCGCTTCTTAGCATGAAGTGTGTGGGGATTTGCAGAAGCAACAGGA 10416

Qy 961 AACCCATGCACTGTGAATCTAGGATTTATTTCAAAAACAAAGG 1001  
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RESULT 2  
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LOCUS AR342806 15418 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1 from patent US 6576464.  
ACCESSION AR342806  
VERSION AR342806.1 GI:33738009  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15418)  
AUTHORS Gold,J.D. and Lebkowski,J.S.  
TITLE Methods for providing differentiated stem cells  
JOURNAL Patent: US 6576464-A 1 10-JUN-2003;  
Geron Corporation; Menlo Park, CA  
FEATURES  
source 1. .15418  
/organism="unknown"  
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ORIGIN  
Query Match 100.0%; Score 1001; DB 6; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 9.1e-272;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 9500 AAAAGACCCAGCATTTGGCACCCCTGGACATTTGCCACAGCCCTGGGAATTCACGCTGAC 9559

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Db 9560 TAGCGACATCATGTATACACTCCCGTCCACAGCCGACCCCGCTGTTTATTTTAAATAGC 9619

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Db 9620 TACAAGCAGGGAATTCCTGCTTAAATGTCTTTTAAACAACTGGTTTAAACAAACGGGTC 9679

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Qy 241 GGCATCTCAAGGGAATTAACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 300  
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Qy 361 TGGGGGCGACGCTGGGGGCTACTGCACGACCTTTTACTTAAAGCCAGTTTCTCGTTCT 420  
Db 9860 TGGGGGCGACGCTGGGGGCTACTGCACGACCTTTTACTTAAAGCCAGTTTCTCGTTCT 9919

Qy 421 GATGGTATTGGCTCAGTTATGGGAGACTAACCATAGGGGAGTGGGATGGGGGAAACCCGG 480  
Db 9920 GATGGTATTGGCTCAGTTATGGGAGACTAACCATAGGGGAGTGGGATGGGGGAAACCCGG 9979

Qy 481 AGGCTGTGCCATCTTTTGGCATGCCGAGTGTCTTGGGACGAGTAATGCTCTAGAGATGCC 540

Db 9980 AGGCTGTGCCATCTTTGGCCATGCGCCGAGTGTCTCTGGGAGGATAATGCTTAGAGATGCC 10039  
Qy 541 CACGCTCTGATTTCCGCCAACTCTGTGACAGAAACCCGCGCCGCCGCCAGGGCTTTTGCAGG 600  
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LOCUS AR490112 15418 bp DNA linear PAT 15-MAY-2004  
DEFINITION Sequence 1 from patent US 6713055.  
ACCESSION AR490112  
VERSION AR490112.1 GI:47257268  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15418)  
AUTHORS Schiff, J.M.  
TITLE Glycosyltransferase vectors for treating cancer  
JOURNAL Patent: US 6713055-A 1 30-MAR-2004;  
Geron Corporation; Menlo Park, CA  
FEATURES  
source location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 1001; DB 6; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 9.1e-272;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 TACAAAGCAGGGAATCCCTGTAATATGCTTTTAAACAACTGGTTTAAACAAACGGGTC 180  
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Qy 181 CATCCGACGGTGGACAGTTCCTCACAGTGAAGAGGACATGCGCGTTTATAAAGCCTGCA 240

Db 9680 CATCCGACCGTGGACAGTTCCTCACAGTGAAGAGGAACATGCGCGTTTATAAAGCCTGCA 9739  
Qy 241 GGCATCTCAAGGGAATTTACGCTGAGTCAAAACCTCCACCTCCATCGGATACGTACGCAAC 300  
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## RESULT 4

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LOCUS AR576878 15418 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 1 from patent US 6777203.  
ACCESSION AR576878  
VERSION AR576878.1 GI:56579198  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15418)  
AUTHORS Morin, G.B.; Lichtsteiner, S.P.; Vasserot, A.P.; Adams, R.R. and Andrews, W.H.  
TITLE Telomerase promoter driving expression of therapeutic gene sequences  
JOURNAL Patent: US 6777203-A 1 17-AUG-2004;  
Geron Corporation; Menlo Park, CA

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ORIGIN
100.0%; Score 1001; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 9.1e-272;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAGACCCAGCAATGGCCAGCCCTGGACATTTGGCCCAAGCCCTGGGAATTCACGTGAC 60
Db AAAAGACCCAGCAATGGCCAGCCCTGGACATTTGGCCCAAGCCCTGGGAATTCACGTGAC 9559

Qy 61 TAGGCATCATGTACACATCCCGTCCAGACGACCCCGCTGTTTATTTATATAGC 120
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Qy 121 TACAAAGCAGGGAATCCCTGCTAAATGTCTTTTAAACAACTGGTTTAAACAAACGGGTC 180
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Qy 241 GGCATCTCAAGGGAATTTACGCTGAGTCAAACTGGCCACCTCCATGGGATACGTACGCAAC 300
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DEFINITION Sequence 1 from Patent WO0242445.
ACCESSION AX453025
VERSION AX453025.1 GI:21712594
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Gold, J.D. and Leebrowski, J.S.
TITLE Differentiated cells suitable for human therapy
JOURNAL Patent: WO 0242445-A 1 30-MAY-2002;
GERON Corporation (US)
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## RESULT 6

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LOCUS Sequence 1 from Patent WO02053760.  
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ACCESSION AX498409  
VERSION AX498409.1 GI:23343287  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE 1

Irving, J.M. and Lebkowski, J.S.  
Chimeric cytolytic viruses for cancer treatment  
Patent: WO 02053760-A 1 11-JUL-2002;  
Geron Corporation (US)  
Location/Qualifiers

## FEATURES

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Query Match 100.0%; Score 1001; DB 6; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 9.1e-272;  
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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## RESULT 7

AX504952 AX504952 15418 bp DNA linear PAT 27-SEP-2002  
LOCUS Sequence 1 from Patent WO0242468.  
DEFINITION AX504952  
ACCESSION AX504952  
VERSION AX504952.1 GI:23386282  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE 1

Schiff, M.J.  
Glycosyltransferase vectors for treating cancer  
Patent: WO 0242468-A 1 30-MAY-2002;  
Geron Corporation (US)  
Location/Qualifiers

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Sequencing of Human Chromosome 5  
Unpublished  
2 (bases 1 to 161252)  
DOE Joint Genome Institute.  
Direct Submission  
Submitted (14-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: http://www.jgi.doe.gov  
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Project Information  
Center Project Name: 451340  
Center clone name: RPCI-11\_117B23  
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Summary Statistics  
Consensus quality: 148939 bases at least Q40  
Consensus quality: 156608 bases at least Q30  
Consensus quality: 158826 bases at least Q20  
Estimated insert size: 175000; agarose-fp estimation  
Estimated insert size: 160452; sum-of-contigs estimation  
Quality coverage: 7.26 in Q20 bases; agarose-fp estimation  
Quality coverage: 7.92 in Q20 bases; sum-of-contigs estimation.  
\* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.  
\* 1 3008: contig of 3008 bp in length  
\* 3009 3108: gap of unknown length  
\* 3109 9209: contig of 6101 bp in length  
\* 9210 9309: gap of unknown length  
\* 9310 15613: contig of 6304 bp in length  
\* 15614 15713: gap of unknown length  
\* 15714 23243: contig of 7530 bp in length  
\* 23244 39674: gap of unknown length  
\* 39675 60001: contig of 16331 bp in length  
\* 60002 60101: contig of 20227 bp in length  
\* 60102 85303: contig of 25202 bp in length  
\* 85304 85403: gap of unknown length  
\* 85404 117460: contig of 32057 bp in length  
\* 117461 117560: gap of unknown length  
\* 117561 161252: contig of 43692 bp in length.  
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60002..60101  
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ORIGIN

Query Match 100.0%; Score 1001; DB 14; Length 161252;
Best Local Similarity 100.0%; Pred. No. 1.1e-271;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 TACGCACATCATGTACACACTCCCGTCCACAGCCAGCCCGCTGTTTATTTAAATAGC 120
Db 140525 TACGCACATCATGTACACACTCCCGTCCACAGCCAGCCCGCTGTTTATTTAAATAGC 140466

Qy 121 TACAAAGCAGGGAATCCCTGCTAAATGTCTTTTAAACAACTGGTTAAACAAACGGGTC 180
Db 140465 TACAAAGCAGGGAATCCCTGCTAAATGTCTTTTAAACAACTGGTTAAACAAACGGGTC 140406

Qy 181 CATCCGACCGTGACAGTTCCTCACAGTGAAGAGAACATGCCGTTTATTAAGCCCTGCA 240
Db 140405 CATCCGACCGTGACAGTTCCTCACAGTGAAGAGAACATGCCGTTTATTAAGCCCTGCA 140346

Qy 241 GGCATCTCAAGGGAATTAACGTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 300
Db 140345 GGCATCTCAAGGGAATTAACGTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 140286

Qy 301 ATGCTCAAAAAGAAAGAAATTTACCCCATGTCAGGGAGTGGTGGGGGTTAAAGACGG 360
Db 140285 ATGCTCAAAAAGAAAGAAATTTACCCCATGTCAGGGAGTGGTGGGGGTTAAAGACGG 140226

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Db 140225 TGGGGGACGACAGCTGGGGGCTACTGCACGACCTTTTACTAAAGCCAGTTTCTGTTCT 140166

Qy 421 GATGGTATTGCTCAGTTATGGGAGACTAACCATAGGGAGTGGGAGTGGGGAAACCCGG 480
Db 140165 GATGGTATTGCTCAGTTATGGGAGACTAACCATAGGGAGTGGGAGTGGGGAAACCCGG 140106

Qy 481 AGGCTGTGCCATCTTTGCGATCCCGAGTGTCTGGGACAGGATATGCTCTAGAGATGCC 540
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Qy 541 CACGTCTGTGATTCGCCCAAACTGTGGACAGAAACCGCCCGCCCGCCAGGGCCTTTGCAGG 600
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Qy 781 AGCGCTCCAGAGCTGAAAAGCGGGAGAGGACCCCTCCACGGAGCCTTCAGCAGGAA 840
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Qy 841 GGCACGGCTGCGCTTTAGCCCAACAGGCGCCCATGCTGGACCTCCGGCTCCGTGCGATAG 900
Db 139745 GGCACGGCTGCGCTTTAGCCCAACAGGCGCCCATGCTGGACCTCCGGCTCCGTGCGATAG 139686

Qy 901 GAGGCACTCGCGCTGCCCTTCTAGCATGAAGTGTGGGGATTTGCAAGAGCAACAGGA 960
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Db 139625 AACCCATGCACCTGTGAATCTAGGATTTATTTCAAAACAAAGG 139585

RESULT 10
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LOCUS AX003120 5126 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 1 from Patent WO9933998.
ACCESSION AX003120
VERSION AX003120.1 GI:9926982
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Wick,M. and Hagen,G.
TITLE Regulatory dna sequences of the human catalytic telomerase sub-unit
gene, diagnostic and therapeutic use thereof
JOURNAL Patent: WO 9933998-A 1 08-JUL-1999;
WICK MARESA (DE); BAYER AG (DE)
FEATURES
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ORIGIN

Query Match 98.7%; Score 988.4; DB 6; Length 5126;
Best Local Similarity 99.8%; Pred. No. 3e-268;
Matches 1000; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 AAAAGACCCAGCATTTGGACACCCCTGGACATTTGGCCCAACAGCCCTGGGAATTCACGTGAC 60
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Qy 61 TACGCACATCATGTACACACTCCCGTCCACAGCCAGCCCGCTGTTTATTTAAATAGC 120
Db 1139 TACGCACATCATGTACACACTCCCGTCCACAGCCAGCCCGCTGTTTATTTAAATAGC 1198

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Db 1199 TACAAAGCAGGGAATCCCTGCTAAATGTCTTTTAAACAACTGGTTAAACAAACGGGTC 1258

Qy 181 CATCCGACCGTGACAGTTCCTCACAGTGAAGAGAACATGCCGTTTATTAAGCCCTGCA 240
Db 1259 CATCCGACCGTGACAGTTCCTCACAGTGAAGAGAACATGCCGTTTATTAAGCCCTGCA 1318

Qy 241 GGCATCTCAAGGGAATTAACGTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 300
Db 1319 GGCATCTCAAGGGAATTAACGTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 1378

Qy 301 ATGCTCAAAAAGAAAGAAATTTACCCCATGTCAGGGAGTGGTGGGGGTTAAAGACG 359
Db 1379 ATGCTCAAAAAGAAAGAAATTTACCCCATGTCAGGGAGTGGTGGGGGTTAAAGACG 1438

Qy 360 GTGGGGGACGACGTGGGGGCTACTGCAACCTTTTAAAGCCAGTTTCTGTTTC 419
Db 1439 GTGGGGGACGACGTGGGGGCTACTGCAACCTTTTAAAGCCAGTTTCTGTTTC 1498

Qy 420 TGATGGTATTGGCTCAGTTATGGGAGACTAACCATAGGGAGTGGGAGAACCCG 479
Db 1499 TGATGGTATTGGCTCAGTTATGGGAGACTAACCATAGGGAGTGGGAGAACCCG 1558

Qy 480 GAGGCTGTGCCATCTTTGGCCATGCCAGTGTCTGGGACAGATAATGCTCTAGAGATGC 539
Db 1559 GAGGCTGTGCCATCTTTGGCCATGCCAGTGTCTGGGACAGATAATGCTCTAGAGATGC 1618

Qy 540 CCAGCTCTGATTTCCCCAAACCTGTGGACAGAAACCCGCCGCCAGGGCCTTTGCAAG 599
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RESULT 11  
AX003122  
LOCUS AX003122 11276 bp DNA linear PAT 24-AUG-2000  
DEFINITION Sequence 3 from Patent W09933998.  
ACCESSION AX003122  
VERSION AX003122.1 GI:9926984  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Wick,M. and Hagen,G.  
TITLE Regulatory dna sequences of the human catalytic telomerase sub-unit  
gene, diagnostic and therapeutic use thereof  
JOURNAL Patent: W0 9933998-A 3 08-JUL-1999;  
WICK MARESA (DE); BAYER AG (DE)  
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ORIGIN

Query Match 98.7%; Score 988.4; DB 6; Length 11276;  
Best Local Similarity 99.8%; Pred. No. 3.3e-268;  
Matches 1000; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
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Db 7409 CATCCGACGGTGGACAGTTCTCTCACAGTGAAGAGGAACATGCCGTTTATAAGACCTGCA 7468  
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Qy 480 GAGGCTGTGCCATCTTTGCCATGCGCGAGTGTCTTGGGCAAGGATATATGCTCTAGAGATGC 539  
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RESULT 12  
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LOCUS AF114847 12213 bp DNA linear PRI 21-SEP-2000  
DEFINITION Homo sapiens telomerase reverse transcriptase (TERT) gene, partial cds.  
ACCESSION AF114847  
VERSION AF114847.1 GI:4324972  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 12213)  
AUTHORS Wu,K.J., Grandori,C., Amacker,M., Simon-Vermot,N., Polack,A.,  
Lingner,J. and Dalla-Pavera,R.  
TITLE Direct activation of TERT transcription by c-MYC

JOURNAL Nat. Genet. 21 (2), 220-224 (1999)  
PUBMED 9988278  
REFERENCE 2 (bases 1 to 12213)  
AUTHORS Duceat, A.-L., Amacker, M., Reichenbach, P., Nabholz, M. and Lingner, J.  
TITLE Identification of the human telomerase reverse transcriptase (hTERT) promoter  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 12213)  
AUTHORS Sutorisz, H., Palmquist, R., Roos, G., Stenling, R., Schorderet, D., Reddel, R., Lingner, J. and Nabholz, M.  
TITLE Rearrangements of minisatellites in the human telomerase reverse transcriptase gene are not correlated with its expression in colon carcinomas  
JOURNAL Unpublished  
REFERENCE 4 (bases 1 to 12213)  
AUTHORS Anacker, M., Simon-Vermot, N. and Lingner, J.  
TITLE Direct Submission  
JOURNAL Submitted (17-DEC-1998) Telomerase Research Unit, ISREC, Chemin de Boveresses 155, Epalinges 1066, Switzerland  
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ORIGIN  
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Best Local Similarity 99.8%; Pred. No. 3.3e-268;  
Matches 1000; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 1 AAAAGACCCAGCATGTGGACACCCCTGGACATTTGGCCCAAGCCCTGGGAATTCACGTGAC 60  
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DB 3702 ATGCTCAAAAAGAAAGAAATTTACCCCATGCGAGGGAGTGGTTAAGGGGGTTAAGGACG 3761  
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Db 4182 AAGCGCTCCAGAGCTG3AAAAAGCGGGGAAGGACCCCTCCACGAGGCTGACAGGGA 4241  
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Qy 900 GGAGGGCACTCGCGCTGCCCTTCTAGCATGAAGTGTGTGGGATTTTCAGAACCAAGG 959  
Db 4302 GGAGGGCACTCGCGCTGCCCTTCTAGCATGAAGTGTGTGGGATTTTCAGAACCAAGG 4361  
Qy 960 AAACCCATGCATGTGAATCTAGGATTTATTTCAAAAACAAAGG 1001  
Db 4362 AAACCCATGCATGTGAATCTAGGATTTATTTCAAAAACAAAGG 4403

RESULT 13  
HSTERT1  
LOCUS Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6.  
DEFINITION AFI28893.1 GI:4808970  
ACCESSION AFI28893  
VERSION 1 of 2  
KEYWORDS Homo sapiens (human)  
SEGMENT  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 26414)  
AUTHORS Wick, M., Zubov, D. and Hagen, G.  
TITLE Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT)  
JOURNAL Gene 232 (1), 97-106 (1999)  
PUBMED 1033526  
REFERENCE 2 (bases 1 to 26414)  
AUTHORS Wick, M., Zubov, D. and Hagen, G.  
TITLE Direct Submission  
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DEFINITION    Sequence 30 from patent US 6492171.
ACCESSION     AR266023
VERSION       AR266023.1 GI:29694869
KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 51552)
AUTHORS       Monia,B.P., Gaarde,W.A., Freier,S.M. and Wanciewicz,E.
TITLE         Antisense modulation of TERT expression
JOURNAL       Patent: US 6492171-A 30 10-DEC-2002;
              ISIS Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES     Location/Qualifiers
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               /mol_type="genomic DNA"
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Query Match      98.7%; Score 988.4; DB 6; Length 51552;
Best Local Similarity 99.8%; Pred. No. 3.8e-268;
Matches 1000; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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QY      61 TAGCACATCATGTACACACTCCGCTCCAGCAGCCGCCCGCTGTTTATTTTAAATAGC 120
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QY      121 TACAAGCAGGAAATCCCTGCTAAATGTCCTTTAACAACACTGTTTAAACAACAGCGGTC 180
DB      7349 TACAAGCAGGAAATCCCTGCTAAATGTCCTTTAACAACACTGTTTAAACAACAGCGGTC 7408
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QY      241 GGCATCTCAAGGGAAATACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 300
DB      7469 GGCATCTCAAGGGAAATACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 7528
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DB      7529 ATGCTCAAAAAGAAATTTACCCCATGCGAGCGAGTGCTTTAGGGGGGTTTAAAGACG 7588
QY      360 GTGGGGGCGAGCGTGGGGGCTACTGACGACACCTTTTACTAAGCCAGATTTCCTGTTTC 419
DB      7589 GTGGGGGCGGCGAGCTGGGGGCTACTGACGACACCTTTTACTAAGCCAGATTTCCTGTTTC 7648
QY      420 TGATGGTATTGGCTCAGTTATGGGAGACTAACCATAGGGGAGTGGGATGGGGGAAACCCG 479
DB      7649 TGATGGTATTGGCTCAGTTATGGGAGACTAACCATAGGGGAGTGGGATGGGGGAAACCCG 7708
QY      480 GAGGCTGTGCCATCTTTTGGCATGCCCAGTGTCTCTGGGACAGATAAATGCTCTAGATGTC 539
DB      7709 GAGGCTGTGCCATCTTTTGGCATGCCCAGTGTCTCTGGGACAGATAAATGCTCTAGATGTC 7768
QY      540 CCAGTCTCTGATTCCTCCCAACCTGTGGACAGAACCCCGCCGCGCCAGGCGCTTTTCAG 599
DB      7769 CCAGTCTCTGATTCCTCCCAACCTGTGGACAGAACCCCGCCGCGCCAGGCGCTTTTCAG 7828
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DB      7829 GTGTGATCTCCGTGAGGACCTCTGAGTCTGCGGATCTTTCGGGACTACCTCGCAGGCCCGAA 7888
QY      660 AAGTAATCCAGGGGTTCTGGGAAGAGCGCGGACAGAGGGTTCAGAGGGGGGAGCCTCAGG 719
DB      7889 AAGTAATCCAGGGGTTCTGGGAAGAGCGCGGACAGAGGGTTCAGAGGGGGGAGCCTCAGG 7948
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QY      720 ACGATGAGGACGCTCAGTCTGAGCTGAAAAGAGGAGGAGGCTCGAGCCCGAGCTGC 779
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QY      840 AGGCACGCGCTGGCCCTTTAGCCACACGAGGCGCCATCGTGGACCTCCCGGCTCCGTCGCA 899
DB      8069 AGGCACGCGCTGGCCCTTTAGCCACACGAGGCGCCATCGTGGACCTCCCGGCTCCGTCGCA 8128
QY      900 GGAGGCGCACTCGCGCTGCCCTTTAGCATCAAGTGTGTGGGATTTTCAGAGCAACAGG 959
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DEFINITION    Homo sapiens chromosome 5 clone CTD-3080P12, complete sequence.
ACCESSION     AC114291
VERSION       AC114291.2 GI:28973811
KEYWORDS      HTG.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiidae; Homo.
REFERENCE     1 (bases 1 to 202305)
AUTHORS       DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE         Direct Submission
JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 202305)
AUTHORS       DOE Joint Genome Institute.
TITLE         Direct Submission
JOURNAL       Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
              Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE     3 (bases 1 to 202305)
AUTHORS       DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE         Direct Submission
JOURNAL       Submitted (15-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
              Drive, Walnut Creek, CA 94598, USA
COMMENT       On Mar 15, 2003 this sequence version replaced gi:19224940.
              Draft Sequence produced by DOE Joint Genome Institute
              www.jgi.doe.gov
              Finishing Completed at Stanford Human Genome Center
              www-sngc.stanford.edu
              Quality: Phrap Quality >=40 99.9% of Sequence;
              Estimated Total Number of Errors is 0.2.
              NOTE: Transposon sequencing failed to verify number of repeat
              copies 173000-175780. Unsure number of repeat copies 173000-175780.
              BAC and subclones unstable 76080. Force join at 76080.
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               /clone="CTD-3080P12"
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              misc_feature
               /note="NOTE: BAC and subclones unstable 76080. Force join
               at 76080."
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               of repeat copies 173000-175780. Unsure number of repeat
               copies 173000-175780"
ORIGIN
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Query Match 98.7%; Score 988.4; DB 8; Length 202305;  
Best Local Similarity 99.8%; Pred. No. 4.3e-268;  
Matches 1000; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 1 AAAGACCCAGCATTTGGACACCCCTGGACATTTGGCCCAACAGCCCTGGGAATTCACGTGAC 60
DB 183042 AAAGACCCAGCATTTGGACACCCCTGGACATTTGGCCCAACAGCCCTGGGAATTCACGTGAC 182983

QY 61 TAGCACATCATGTACACATCCCGTCCAGACCCGCGCTGTTTATTTTAAATAGC 120
DB 182982 TAGCACATCATGTACACATCCCGTCCAGACCCGCGCTGTTTATTTTAAATAGC 182923

QY 121 TACAAGCAGGGAATCCCTGCTAAATGTCTTTAACTGTTTAAACAAACGGGTC 180
DB 182922 TACAAGCAGGGAATCCCTGCTAAATGTCTTTAACTGTTTAAACAAACGGGTC 182863

QY 181 CATCCGCAACGGTGACAGTTCTCTCACAGTGAAGAGGAACATGCGTTTATAAAGCCTGCA 240
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QY 241 GGCATCTCAAGGGAATTTACGCTGAGTCAAACTGCCACCTCCATGGGATACGTACGCAAC 300
DB 182802 GGCATCTCAAGGGAATTTACGCTGAGTCAAACTGCCACCTCCATGGGATACGTACGCAAC 182743

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QY 360 GTGGGGCAGCAGCTGGGGGCTACTGCAACACCTTTTACTAAAGCCAGTTTCTTGTTTC 419
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QY 420 TGATGGTATTGGCTCAGTTATGGAGACTAACCATAGGGGAGTGGGATGGGGGAACCCG 479
DB 182622 TGATGGTATTGGCTCAGTTATGGAGACTAACCATAGGGGAGTGGGATGGGGGAACCCG 182563

QY 480 GAGCTGTGTCATCTTTGCCATGCCGAGTGTCTGGGCAGAGGATATGCTCTAGAGATGC 539
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QY 600 GTGTGATCTCCGTGAGGACCTCAGGTCTGGGATCCTTCGGGACTACCTGACGGCCCGAA 659
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QY 660 AAGTAATCCAGGGGTTCTGGGAAGAGCGGGCAGAGGGGTACAGAGGGGGCAGCCTCAGG 719
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QY 720 ACGATGAGGACAGTCAAGTCTGAGGCTGAAGGGGAGGGGCTTCGAGCCAGGGCTGC 779
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QY 780 AAGCGCTCCAGAACTGGAAGAAAGCGGGGAAGGACCTTCCACGGAGCCTGACAGCAGGA 839
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QY 900 GGAGGGCACTCGCGCTGCCCTTTCTAGCATGAAGTGTGTGGGGATTTGCAGAAAGCAACAGG 959
DB 182142 GGAGGGCACTCGCGCTGCCCTTTCTAGCATGAAGTGTGTGGGGATTTGCAGAAAGCAACAGG 182083

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Job time : 5393 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 10:27:39 ; Search time 205 seconds  
(without alignments)  
8679.704 Million cell updates/sec

Title: US-09-615-039-1\_COPY\_9500\_10500

Perfect score: 1001

Sequence: 1 aaagaccagcattgac.....ggattattcaaaacaagg 1001

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgm2\_6/ptodata/1/ina/1 COMB.seq:\*
- 2: /cgm2\_6/ptodata/1/ina/5 COMB.seq:\*
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- 4: /cgm2\_6/ptodata/1/ina/6B COMB.seq:\*
- 5: /cgm2\_6/ptodata/1/ina/H COMB.seq:\*
- 6: /cgm2\_6/ptodata/1/ina/PCTUS COMB.seq:\*
- 7: /cgm2\_6/ptodata/1/ina/PP COMB.seq:\*
- 8: /cgm2\_6/ptodata/1/ina/RE COMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1001	100.0	15418	3	US-09-244-438-1
4	1001	100.0	15418	3	US-09-995-419A-1
5	988.4	98.7	51552	3	US-09-733-294A-30
6	50.2	5.0	25589	3	US-09-949-002-716
7	49.2	4.9	32177	3	US-09-949-002-712
8	49	4.9	7218	2	US-08-232-463-14
9	48.2	4.8	93493	3	US-09-949-016-12063
10	48.2	4.8	95020	3	US-09-949-016-13272
11	48	4.8	601	3	US-09-949-016-19450
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13	48	4.8	601	3	US-09-949-016-49663
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24	46.8	4.7	126200	3	US-09-949-016-13193

ALIGNMENTS

RESULT 1

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; Sequence 1, Application US/09783203  
; Patent No. 6576464  
; GENERAL INFORMATION:  
; APPLICANT: Geron Corporation  
; APPLICANT: Gold, Joseph  
; APPLICANT: Lebkowski, Jane  
; TITLE OF INVENTION: Tpacked stem cells  
; FILE REFERENCE: 096/003  
; CURRENT APPLICATION NUMBER: US/09/783,203  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: 60/253,443  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/253,357  
; PRIOR FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 15418  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-783-203-1

Query Match	100.0%	Score 1001;	DB 3;	Length 15418;
Best Local Similarity	100.0%	Pred. No. 2.6e-307;	Mismatches 0;	Indels 0;
Matches 1001;	Conservative 0;			Gaps 0;
Qy	1	AAAAGACCAGCATTGGCACCCTTGGACATTTGCCACACAGCCCTTGGGAATTCAGTGAC	60	
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Qy	301	ATGCTCAAAGAAAGAAATTTTCACCCATGGCAGGGAGTGTTGGGGGTTTAAGGACGG	360
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Qy	421	GATGGTATTGGCTCAGTTATGGAGAGTAACNATAGGGAGTGGGATGGGGGAACCCGG	480
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Qy	481	AGGCTGTGCCATCTTTGGCCATGCCGAGTGTCTTGCGCAGGATAATGCTTAGAGATGCC	540
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Qy	541	CAGTCTCTGATTTCCCCCAACCTGTGGACAGAACCCGCCGCCCGCCCTTTGCGAGG	600
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RESULT 2
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; Sequence 1, Application US/09994427A
; Patent No. 6713055
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
; FILE REFERENCE: 083,002
; CURRENT APPLICATION NUMBER: US/09/994,427A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 60/253,395
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-994-427A-1

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Query Match 100.0%; Score 1001; DB 3; Length 15418;  
Best Local Similarity 100.0%; Pred. No. 2.6e-307;



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Db	10220	CGATGGAGGCACTCAGTCTGAGGCTGAAAAAGGAGGAGGGGCTTCGAGCCACAGGCGCTGCA	10279	
Qy	781	AGCGCTCCAGAACTGGGAAAAGCGGGGAGGGACCTTCCACGAGAGCTTCGACGACGAA	840	
Db	10280	AGCGCTCCAGAACTGGGAAAAGCGGGGAGGGACCTTCCACGAGAGCTTCGACGACGAA	10339	
Qy	841	GGCAGCGCTGGCCCTTAGGCCACCAAGGGCCATCGTGGACCTCCCGCTCCGTTGCCATAG	900	
Db	10340	GGCAGCGCTGGCCCTTAGGCCACCAAGGGCCATCGTGGACCTCCCGCTCCGTTGCCATAG	10399	
Qy	901	GAGGGCACTCGCGCTGCCCTTCTAGCATGAAGTGTGTGGGANTTGCAGAGCAACAGGA	960	
Db	10400	GAGGGCACTCGCGCTGCCCTTCTAGCATGAAGTGTGTGGGANTTGCAGAGCAACAGGA	10459	
Qy	961	AACCCATGCACTGTGAATCTAGGATATTTCAAAACAAAGG	1001	
Db	10460	AACCCATGCACTGTGAATCTAGGATATTTCAAAACAAAGG	10500	
RESULT 4				
US-09-995-419A-1				
; Sequence 1, Application US/09995419A				
; Patent No. 6921665				
; GENERAL INFORMATION:				
; APPLICANT: Geron Corporation				
; APPLICANT: McWhir, Jim				
; APPLICANT: Gold, Joseph D.				
; APPLICANT: Schiff, J. Michael				
; TITLE OF INVENTION: 096,004 - Seglist				
; FILE REFERENCE: 096,004 - Seglist				
; CURRENT APPLICATION NUMBER: US/09/995,419A				
; CURRENT FILING DATE: 2001-11-26				
; PRIOR APPLICATION NUMBER: 60/253,357				
; PRIOR FILING DATE: 2000-11-27				
; NUMBER OF SEQ ID NOS: 20				
; SOFTWARE: PatentIn version 3.1				
; SEQ ID NO 1				
; LENGTH: 15418				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-09-995-419A-1				
Query Match 100.0%; Score 1001; DB 3; Length 15418;				
Best Local Similarity 100.0%; Fred. No. 2.6e-307;				
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	AAAGACCCAGCATTTGGCACCCCTTGACATTTGCCCCACAGCCCTGGGAATTCAGGTGAC	60	
Db	9500	AAAGACCCAGCATTTGGCACCCCTTGACATTTGCCCCACAGCCCTGGGAATTCAGGTGAC	9559	
Qy	61	TACGCACATCATGTACACATCTCCCGTCCACGACGACCCCGCTGTTTTATTTAATAGC	120	
Db	9560	TACGCACATCATGTACACATCTCCCGTCCACGACGACCCCGCTGTTTTATTTAATAGC	9619	
Qy	121	TACAAAGCAGGGAATCCCTGTCTTTAAATGCTCTTTAAACAACTGTTAAACAAACGGGTC	180	
Db	9620	TACAAAGCAGGGAATCCCTGTCTTTAAATGCTCTTTAAACAACTGTTAAACAAACGGGTC	9679	
Qy	181	CATCCGACGCTGGACAGTTCTCTCACAGTGAAGAGGAACATGCCGTTTATAAAGCCTGCA	240	
Db	9680	CATCCGACGCTGGACAGTTCTCTCACAGTGAAGAGGAACATGCCGTTTATAAAGCCTGCA	9739	
Qy	241	GGCATCTCAAGGGAATTAACGCTGAGTCAAAATCGCCACCTCCATGGGATACGTACGCAAC	300	
Db	9740	GGCATCTCAAGGGAATTAACGCTGAGTCAAAATCGCCACCTCCATGGGATACGTACGCAAC	9799	
Qy	301	ATGCTCAAAAGAAAGAAATTTACCCCATGGCAGGGAGTGGTTGGGGGGTTAAGACGG	360	
Db	9800	ATGCTCAAAAGAAAGAAATTTACCCCATGGCAGGGAGTGGTTGGGGGGTTAAGACGG	9859	



LOCATION: (42944)...(46129)  
; OTHER INFORMATION: intron 13  
; NAME/KEY: exon  
; LOCATION: (46130)...(46254)  
; OTHER INFORMATION: exon 14  
; NAME/KEY: intron  
; LOCATION: (46255)...(47035)  
; OTHER INFORMATION: intron 14  
; NAME/KEY: exon  
; LOCATION: (47036)...(47173)  
; OTHER INFORMATION: exon 15  
; NAME/KEY: intron  
; LOCATION: (47174)...(47709)  
; OTHER INFORMATION: intron 15  
; NAME/KEY: exon  
; LOCATION: (47710)...(50544)  
; OTHER INFORMATION: exon 16  
US-09-733-294A-30

Query Match 98.7%; Score 988.4; DB 3; Length 51552;  
Best Local Similarity 99.8%; Pred. No. 5.2e-303; Indels 1; Gaps 1;  
Matches 1000; Conservative 0; Mismatches 1;

Qy 1 AAAGACCCAGCATTTGGCACCCCTGGACATTTGGCCACACAGCCCTGGGAATTCAGTGC 60  
Db 7229 AAAGACCCAGCATTTGGCACCCCTGGACATTTGGCCACACAGCCCTGGGAATTCAGTGC 7288

Qy 61 TAGCACATCATGATACACATCTCCGTCACAGCCGACCCCGCTGTTTATTTAATAGC 120  
Db 7289 TAGCACATCATGATACACATCTCCGTCACAGCCGACCCCGCTGTTTATTTAATAGC 7348

Qy 121 TACAAGCAGGGAATCCCTGCTAAATGTCCTTTTACAACTGTTTAAACAAACGGGTC 180  
Db 7349 TACAAGCAGGGAATCCCTGCTAAATGTCCTTTTACAACTGTTTAAACAAACGGGTC 7408

Qy 181 CATCCGACGGTGACAGTCTCTCACAGTGAAGAGAACATGCCGCTTTTATAAGCCCTGCA 240  
Db 7409 CATCCGACGGTGACAGTCTCTCACAGTGAAGAGAACATGCCGCTTTTATAAGCCCTGCA 7468

Qy 241 GGCATCTCAAGGGAATTAAGTGTAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 300  
Db 7469 GGCATCTCAAGGGAATTAAGTGTAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 7528

Qy 301 ATGCTCAAAAGAAAGAAATTTACCCCATGCGAGGGAGTGTTTGGGGGTTAAGACG 359  
Db 7529 ATGCTCAAAAGAAAGAAATTTACCCCATGCGAGGGAGTGTTTGGGGGTTAAGACG 7588

Qy 360 GTGGGGGACGACGCTGGGGGCTACTGACGACACCTTTTACTAAAGCCAGTTTCTGGTTC 419  
Db 7589 GTGGGGGACGACGCTGGGGGCTACTGACGACACCTTTTACTAAAGCCAGTTTCTGGTTC 7648

Qy 420 TGATGGTATTGGCTCAGTTATGGAGACTAAACATAGGGAGTGGGATGGGGAAACCCG 479  
Db 7649 TGATGGTATTGGCTCAGTTATGGAGACTAAACATAGGGAGTGGGATGGGGAAACCCG 7708

Qy 480 GAGCTGTGCCATCTTTGCCATGTCGAGTGTCTGGCAGAGTAATGCTCTAGAGTGC 539  
Db 7709 GAGCTGTGCCATCTTTGCCATGTCGAGTGTCTGGCAGAGTAATGCTCTAGAGTGC 7768

Qy 540 CCAGTCTGATTTCCCCCAACCTGTGGACAGAACCCGCGCCGCCAGGCGCTTTTGAG 599  
Db 7769 CCAGTCTGATTTCCCCCAACCTGTGGACAGAACCCGCGCCGCCAGGCGCTTTTGAG 7828

Qy 600 GTGTGATCTCCGTGAGGACCTTGAGTCTGGGATCTTTGGGACTTACCTGAGGCCCGAA 659  
Db 7829 GTGTGATCTCCGTGAGGACCTTGAGTCTGGGATCTTTGGGACTTACCTGAGGCCCGAA 7888

Qy 660 AAGTAATCCAGGGTTCTGGGAAGAGGCGGCGCAGAGGCTCAGAGGGGGCAGCTCAGG 719  
Db 7889 AAGTAATCCAGGGTTCTGGGAAGAGGCGGCGCAGAGGCTCAGAGGGGGCAGCTCAGG 7948

Qy 720 ACGATGAGGAGTCAAGTCTCAGGCTGAAAGGGAGGGAGGCGCTTCAGGCCAGGCTGC 779

Db 7949 ACGATGAGGAGTCAAGTCTCAGGCTGAAAGGGAGGGGCTCGAGCCAGGCTGC 8008

Qy 780 AAGCGCTCCAGAGCTTGGAAAGCGGGAAGGGACCTCCACGAGCCTGCAGCAGGA 839

Db 8009 AAGCGCTCCAGAGCTTGGAAAGCGGGAAGGGACCTCCACGAGCCTGCAGCAGGA 8068

Qy 840 AAGCAGCGCTGGCCCTTTAGCCACACGAGGCGCCATCGTGGACCTCCCGCCTCCGTCAT 899

Db 8069 AAGCAGCGCTGGCCCTTTAGCCACACGAGGCGCCATCGTGGACCTCCCGCCTCCGTCAT 8128

Qy 900 GAGGGCAGCTCGCGCTCCCTTTCAGCATGAAGTGTGTGGGATTTTCAGAGCAACAGG 959

Db 8129 GAGGGCAGCTCGCGCTCCCTTTCAGCATGAAGTGTGTGGGATTTTCAGAGCAACAGG 8188

Qy 960 AAACCCATGCATGTGAATCTAGGATTTATTTCAAAACAAAGG 1001

Db 8189 AAACCCATGCATGTGAATCTAGGATTTATTTCAAAACAAAGG 8230

## RESULT 6

US-09-949-002-716/c  
; Sequence 716, Application US/09949002  
; Patent No. 6900016  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000790  
; CURRENT APPLICATION NUMBER: US/09/949,002  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/231,401  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 10823  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 716  
; LENGTH: 25589  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(25589)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-002-716

Query Match 5.0%; Score 50.2; DB 3; Length 25589;  
Best Local Similarity 54.5%; Pred. No. 0.00017;  
Matches 164; Conservative 0; Mismatches 133; Indels 4; Gaps 3;

Qy 591 CCTTTGCAAGTGTGATCTCGTGAGGACCTCGAGGTCTGGGATCTTCGGGACTACCTGC 650  
Db 927 CCTTGGCAGATATGATTAATTAAGATCTTGACAGAGAGCTATCTGGATTATCTGG 868

Qy 651 AGGCCCGAAAGTAATCCAGGGGTTCTGGGAAGAGCGGGCAGGAGGTTCAGAGGGGGC 710  
Db 867 TGGACC-CAGTGTAAATCAGAGGGGCTTTATTAGAGGAGGCAAAAGGTTCAGAGTCAAGG 809

Qy 711 AG-CCTCAGGACGATGAGGAGTCAAGTCTGAGGCTGAAAAGG--GAGGGAGGGCTCGA 767  
Db 808 AGATGTCAATGAAAGCAAAAGGTTCAGAGTGTATGATGCTGTGAAAGAGGACATGA 749

Qy 768 GCCCAGCGCTGACAGCCCTCCAGAGCTGGAAAAGCGGGAGGGACCTCCACCGAG 827  
Db 748 GCCAAGGAGCAGATGGCTCTTAGAACTAGAAAAGAGAGAAACAGATTCTCTTTAGG 689

Qy 828 CCTCAGCAGGAAGGACGCGCTGGCCCTTAGCCACCCAGGGGCCCATCGTGGACCTCCGGC 887  
Db 688 CCTCAGGAAGAACACACACACTTTGATTTAGCTGATAGGACACATTTTGGACTTCTGT 629

Qy 888 C 888  
Db 628 C 628



Query Match 4.8%; Score 48.2; DB 3; Length 93493;  
Best Local Similarity 56.2%; Pred. No. 0.0015;  
Matches 131; Conservative 0; Mismatches 98; Indels 4; Gaps 2;  
  
Qy 581 GGCCTCCAGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 640  
Db 22975 GGCCTCCAGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 640  
  
Qy 641 GACTACTCTGAGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 700  
Db 22975 GGCCTCCAGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 700  
  
Qy 701 AGAGGGGGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 22858  
Db 22975 GGCCTCCAGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 22858  
  
Qy 701 AGAGGGGGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 760  
Db 22975 GGCCTCCAGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 760  
  
Qy 761 G--CCTGAGCGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 811  
Db 22797 GAACCAAGACGAGGATGCGATGCTTACCAAGCTGGAATGGAAGGAA 22745

RESULT 10  
US-09-949-016-13272/c  
; Sequence 13272, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13272  
; LENGTH: 95020  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-13272

Query Match 4.8%; Score 48.2; DB 3; Length 95020;  
Best Local Similarity 56.2%; Pred. No. 0.0015;  
Matches 131; Conservative 0; Mismatches 98; Indels 4; Gaps 2;  
  
Qy 581 GGCCTCCAGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 640  
Db 23633 GGCCTCCAGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 640  
  
Qy 641 GACTACTCTGAGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 700  
Db 23573 GACTACTCTGAGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 700  
  
Qy 701 AGAGGGGGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 760  
Db 23515 CGAGTAATGAGCATGAGACGACCCCGGTAGCTATTGCTGCTTTGAGATAGGAGAG 23456  
  
Qy 761 G--CCTGAGCGGCGCTTTCAGGTGATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 811  
Db 23455 GAACCAAGACGAGGATGCGATGCTTACCAAGCTGGAATGGAAGGAA 23403

RESULT 11  
US-09-949-016-19450/c  
; Sequence 19450, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19450  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-19450

Query Match 4.8%; Score 48; DB 3; Length 601;  
Best Local Similarity 70.0%; Pred. No. 0.0001;  
Matches 63; Conservative 1; Mismatches 26; Indels 0; Gaps 0;  
  
Qy 751 GGGAGGAGGCGCTTCGAGCCCGGCTGCAAGCGCTTCCAGAGCTCCAGAGCTGGAAGGGA 810  
Db 310 GGAAGGAGGCGCTTCGAGCCCGGCTGCAAGCGCTTCCAGAGCTTCCAGAGCTGGAAGGGA 251  
  
Qy 811 AGGAGCCCTCCAGGCGCTTCCAGAGCTTCCAGAGCTTCCAGAGCTTCCAGAGCTTCCAGAGGAA 840  
Db 250 AGGAGCTCCCTCCAGGCGCTTCCAGAGCTTCCAGAGCTTCCAGAGCTTCCAGAGGAA 221

RESULT 12  
US-09-949-016-19451/c  
; Sequence 19451, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19451  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-19451

Query Match 4.8%; Score 48; DB 3; Length 601;  
Best Local Similarity 67.3%; Pred. No. 0.0001;  
Matches 66; Conservative 1; Mismatches 31; Indels 0; Gaps 0;  
  
Qy 743 GCTGAAAGGAGGAGGCGCTTCGAGCCCGGCTGCAAGCGCTTCCAGAGCTGGAAGGGA 802  
Db 303 GCTGAAAGGAGGAGGCGCTTCGAGCCCGGCTGCAAGCGCTTCCAGAGCTGGAAGGGA 802  
  
Qy 803 AGCGGGGAGGAGGCGCTTCGAGCCCGGCTGCAAGCGCTTCCAGAGCTGGAAGGGA 840  
Db 243 GCGAGGAGGAGGCGCTTCGAGCCCGGCTGCAAGCGCTTCCAGAGCTGGAAGGGA 206

RESULT 13  
US-09-949-016-49663/c

```

; Sequence 49663, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 49663
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-49663

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	Query Match	4.8%	Score 48	DB 3	Length 601
	Best Local Similarity	70.0%	Pred. No. 0.0001		
	Matches	63	Conservative 1	Mismatches 26	Indels 0
				Gaps 0	
Qy	751	GGAGGAGGGGCTCGAGCCAGCCCTCGAAGCGCCTCCAGAGCTGGAAAAAGCGGGGA	810		
Db	310	GGAAGGAGGKGCCATGAGCCAGGGGATGCGAGCACCTCCAGAGCTGGAAATTGCAGGAA	251		
Qy	811	AGGAGCCCTCCAGGAGCCTGCAGCAGAA	840		
Db	250	AGGGATCTCCCTGGAGCTTCCAGAAAGAA	221		

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RESULT 14
US-09-949-016-49664/c
; Sequence 49664, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49664
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-49664

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	Query Match	4.8%	Score 48;	DB 3;	Length 601;
	Best Local Similarity	67.3%;	Pred. No. 0.0001;		
	Matches	66;	Conservative	1;	Mismatches 31; Indels 0; Gaps 0;
QY	743	GCTGAAGAGGAGGGGCTCGAGCCGAGGCTCGAAGGGCTCCAGAGCTCGAGAA	802		
Db	303	GCYGGCTTGAAGGAGTGCATGAGCCAGGGATGCAAGCACCTCCAGAGCTGGAATT	244		
QY	803	AGCGGGGAGGGACCTCCACGGAGCCTGCAGAGGAA	840		
Db	243	GCACGAAAGGGATCTCCCTGGAGCTTCAGAAAGAA	206		

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RESULT 15
US-09-949-016-13841/c
; Sequence 13841, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13841
; LENGTH: 134008
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(134008)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13841

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	Query Match	4.8%	Score 47.8;	DB 3;	Length 134008;
	Best Local Similarity	56.8%;	Pred. No. 0.0024;		
	Matches	88;	Conservative	0;	Mismatches 67;
					Indels 0;
					Gaps 0;
Qy	691	CAGGAGGCTCAGAGGGGGGCGACCTCAGGACGATGGAGGCAGTCAGTCTGAGGCTGAAAA	750		
Db	55755	CACAAGAGGGATGGGGGGGGCGCTGTATCAGAGGCGGTGAGCTGAGACGGAGGCAGAGGC	55696		
Qy	751	GGAGGGGAGGGGCTCTGAGGCCAGGGCTTCAGAACGCGCTCCAGAACTGTGAAAAAGCGGGGA	810		
Db	55695	TGGGGTGACTCAGGGCTGACCAAGGGGCGAGCGGCTTCAGACGCTGGAGAGGCGGGAA	55636		
Qy	811	AGGGACCCCTCCACGAGGCTGTGACGAGGAAGGCAC	845		
Db	55635	ACGGGGTCTCCCTGGAGCCGCCAGAAAAACCCAC	55601		

Search completed: January 10, 2006, 19:47:31  
Job time : 207 secs

9800 ATGCTCAAAAGAAAGAAATTTACCCCATGGCAGGGGAGTGGTTGGGGG  
 361 TGGGGGAGCAGCTGGGGGCTACTGACGACCTTTTAAAGCCAGTGGGGGTTAAAGACGG 9859  
 9860 TGGGGGAGCAGCTGGGGGCTACTGACGACCTTTTAAAGCCAGTGGGGGTTAAAGACGG 420  
 421 GATGGTATTTGGCTCAGTATAGGAGACTAAACATAGGAGGAGTGGGATCGGTTTCTGTTCT 9919  
 9920 GATGGTATTTGGCTCAGTATAGGAGACTAAACATAGGAGGAGTGGGATCGGTTTCTGTTCT 480  
 481 AGGCTGTGCATCTTTGGCAGTATAGGAGACTAAACATAGGAGGAGTGGGATCGGTTTCTGTTCT 9979  
 9980 AGGCTGTGCATCTTTGGCAGTATAGGAGACTAAACATAGGAGGAGTGGGATCGGTTTCTGTTCT 540  
 541 CAGCTCTCATTTCCCAACCTGTGGACAGAACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 10039  
 10040 CAGCTCTCATTTCCCAACCTGTGGACAGAACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 600  
 601 TGTGATCTCCGTGAGGAGCCCTGAGGCTCTGGGATCTCTCGGGAGTACCCCGAGGCTTTGCAAG 10099  
 10100 TGTGATCTCCGTGAGGAGCCCTGAGGCTCTGGGATCTCTCGGGAGTACCCCGAGGCTTTGCAAG 660  
 661 AGTAATCCAGGGGTTCTGGGAAGAGCGCGGCAAGGGAGGCAGGCTGAGGAGTACCTGAGGAGCCGAA 10159  
 10160 AGTAATCCAGGGGTTCTGGGAAGAGCGCGGCAAGGGAGGCAGGCTGAGGAGTACCTGAGGAGCCGAA 720  
 721 CGATGAGGAGCAGTCTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 10219  
 10220 CGATGAGGAGCAGTCTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
 781 AGCGCTCCAGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 10279  
 781 AGCGCTCCAGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
 10280 AGCGCTCCAGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 10339  
 841 GGCAGCGCTGGCCCTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
 10340 GGCAGCGCTGGCCCTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 10399  
 901 GAGGAGCAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960  
 10400 GAGGAGCAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 10459  
 961 AACCCATGCACTGTGAATCTAGGATTTATTTCAAAACAAAGG 1001  
 10460 AACCCATGCACTGTGAATCTAGGATTTATTTCAAAACAAAGG 10500

RESULT 5

US-10-023-969-1  
 ; Sequence 1, Application US/10023969  
 ; Publication No. US20030095989A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Geron Corporation  
 ; APPLICANT: Irving, John  
 ; APPLICANT: Lebkowski, Jane  
 ; TITLE OF INVENTION: Chimeric Cytolytic Viruses for Cancer Treatment  
 ; FILE REFERENCE: 084,002  
 ; CURRENT APPLICATION NUMBER: US/10/023,969  
 ; PRIOR FILING DATE: 2001-12-17  
 ; PRIOR APPLICATION NUMBER: 60/256,418  
 ; PRIOR FILING DATE: 2000-12-18  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 15418  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-023-969-1

Query Match 100.0%; Score 1001; DB 5; Length 15418;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6

US-10-206-447-1  
 ; Sequence 1, Application US/10206447

1 AAAAGAGCCAGCATTTGGCACCCCTGGACATTTGCCCCACAGCCCTGGGAATTCACCTGAC 60  
 9500 AAAAGAGCCAGCATTTGGCACCCCTGGACATTTGCCCCACAGCCCTGGGAATTCACCTGAC 955  
 61 TACGACACATCATGTACACACTCCCTGTCACGACCGACCCCGCTGTTTAAATATAGC 120  
 9560 TACGACACATCATGTACACACTCCCTGTCACGACCGACCCCGCTGTTTAAATATAGC 961  
 121 TACAAAGCAGGAGAAATCCCTGCTAAATATGTCTTTAAACAACTGTTTAAACAAAGCGGTC 180  
 9620 TACAAAGCAGGAGAAATCCCTGCTAAATATGTCTTTAAACAACTGTTTAAACAAAGCGGTC 967:  
 181 CATCGCACGCTGGACAGTTCCTCAGAGTGAAGAGGAAACATGCCCTTTTAAAGCCTGCA 240  
 9680 CATCGCACGCTGGACAGTTCCTCAGAGTGAAGAGGAAACATGCCCTTTTAAAGCCTGCA 973:  
 241 GGCATCTCAAGGGAAATTTACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 300  
 9740 GGCATCTCAAGGGAAATTTACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 9795  
 301 ATGCTCAAAAGAAAGAAATTTACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 360  
 9800 ATGCTCAAAAGAAAGAAATTTACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 9859  
 361 TGGGGGAGCAGCTGGGGGCTACTGACGACCTTTTAAAGCAGTTCCTGTTCT 420  
 9860 TGGGGGAGCAGCTGGGGGCTACTGACGACCTTTTAAAGCAGTTCCTGTTCT 9919  
 421 GATGGTATTTGGCTCAGTATAGGAGACTAAACATAGGAGGAGTGGGATCGGTTTCTGTTCT 480  
 9920 GATGGTATTTGGCTCAGTATAGGAGACTAAACATAGGAGGAGTGGGATCGGTTTCTGTTCT 9979  
 481 AGGCTGTGCATCTTTGGCAGTATAGGAGACTAAACATAGGAGGAGTGGGATCGGTTTCTGTTCT 540  
 9980 AGGCTGTGCATCTTTGGCAGTATAGGAGACTAAACATAGGAGGAGTGGGATCGGTTTCTGTTCT 1003:  
 541 CAGCTCTCATTTCCCAACCTGTGGACAGAACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 600  
 10040 CAGCTCTCATTTCCCAACCTGTGGACAGAACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 10095  
 601 TGTGATCTCCGTGAGGAGCCCTGAGGCTCTGGGATCTCTCGGGAGTACCCCGAGGCTTTGCAAG 660  
 10100 TGTGATCTCCGTGAGGAGCCCTGAGGCTCTGGGATCTCTCGGGAGTACCCCGAGGCTTTGCAAG 10159  
 661 AGTAATCCAGGGGTTCTGGGAAGAGCGCGGCAAGGGAGGCAGGCTGAGGAGTACCTGAGGAGCCGAA 10219  
 10160 AGTAATCCAGGGGTTCTGGGAAGAGCGCGGCAAGGGAGGCAGGCTGAGGAGTACCTGAGGAGCCGAA 720  
 721 CGATGAGGAGCAGTCTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
 10220 CGATGAGGAGCAGTCTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 10279  
 781 AGCGCTCCAGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
 10280 AGCGCTCCAGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
 841 GGCAGCGCTGGCCCTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960  
 10340 GGCAGCGCTGGCCCTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 10399  
 901 GAGGAGCAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960  
 10400 GAGGAGCAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 10459  
 961 AACCCATGCACTGTGAATCTAGGATTTATTTCAAAACAAAGG 1001  
 10460 AACCCATGCACTGTGAATCTAGGATTTATTTCAAAACAAAGG 10500

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721	CGATGGAGGCAGTCTGCTTGGAGCTCGAAGGGAGGGAGGGCCTCGAGCCAGGCCTCGCA	781	AGCGCCTCCAGAAAGCTGGAAAAAGCGGGAGAGGACCCCTCCACGGAGCCTGACGACGAA	840	
10220	CGATGGAGGCAGTCTGCTTGGAGCTCGAAGGGAGGGAGGGCCTCGAGCCAGGCCTCGCA	10280	AGCGCCTCCAGAGCTGGAAAAAGCGGGAAAGGACCCCTCCACGGAGCCTGACGACGAA	10330	
Qy		Qy		Qy	
Db		Db		Db	
841	GGCAAGGCTGGCCCTTAGCCCAACAGGGCCCATCGTGGACCTCCGGCCCTCCGTGCCATAG	900			
10340	GGCAAGGCTGGCCCTTAGCCCAACAGGGCCCATCGTGGACCTCCGGCCCTCCGTGCCATAG	10390			
Qy		Qy		Qy	
Db		Db		Db	
901	GAGGGCACTGGCGCTGCCCTTCTAGCATGAAGTGTGTGGGGATTTTCAGAGCAACAGGA	960			
10400	GAGGGCACTGGCGCTGCCCTTCTAGCATGAAGTGTGTGGGGATTTTCAGAGCAACAGGA	10450			
Qy		Qy		Qy	
Db		Db		Db	
961	AACCCATGCACTGTGAATCTAGGATTAATTTCAAAACAAAGG	1001			
10460	AACCCATGCACTGTGAATCTAGGATTAATTTCAAAACAAAGG	10500			
Qy		Qy		Qy	
Db		Db		Db	

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RESULT 4
US-10-141-220-1
; Sequence 1, Application US/10141220
; Publication NO. US20030040111AI
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tracked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/10/141,220
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/09/783,203
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-141-220-1

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9800	Db	ATCCTC	AAAGAAGAAATTCACCCCATGCGAGGGAGTGGTGTGGTGGGGGGTTAAGGACGG	9859
361	Qy	TGGGGGCAGCAGCTGGGGGCTACTG	CAGCACCCTTTTACTTAAGCAAAAGCCAGTTTCTCTGGTTCT	420
9860	Db	TGGGGGCAGCAGCTGGGGGCTACTG	CAGCACCCTTTTACTTAAGCAAAAGCCAGTTTCTCTGGTTCT	9919
421	Qy	GATGTTATTTGGCTCAGTTATGGGAGACTAA	CAACATAGGGGAGTGGGGATCGGGGATGGGGGAACCCCG	480
9920	Db	GATGTTATTTGGCTCAGTTATGGGAGACTAA	CAACATAGGGGAGTGGGGATCGGGGGAACCCCG	9979
481	Qy	AGGCTGTGCCATCTTTGCCATGCCCGGAGTGTCT	GTGGGCAGGATAATGCTCTAGAGTAGAGATGCC	540
9980	Db	AGGCTGTGCCATCTTTGCCATGCCCGGAGTGTCT	GTGGGCAGGATAATGCTCTAGAGTAGAGATGCC	1003
541	Qy	CAGTCTCTGATTTCCGCCAAACCTGTGGACAGAA	CCCGCCGCCCCACAGGGCTGGGCTTTGCAGG	600
10040	Db	CAGTCTCTGATTTCCGCCAAACCTGTGGACAGAA	CCCGCCGCCCCACAGGGCTGGGCTTTGCAGG	10099
601	Qy	TCGTGATCTCCGTGAGGACCTGAGGTCTGGGATCT	TCGGGACTACCTGTACCTGCAGGCCCGGAA	660
10100	Db	TGTGATCTCCGTGAGGACCTGAGGTCTGGGATCT	TCGGGACTACCTGTACCTGCAGGCCCGGAA	10151
661	Qy	AGTAATCCAGGGGTTCTGGGAGAGCGCGGCGAGAG	GGTCTCAGAGGGGGGGGGCGACCTTCAGGA	720
10160	Db	AGTAATCCAGGGGTTCTGGGAGAGCGCGGCGAGAG	GGTCTCAGAGGGGGGGGGCGACCTTCAGGA	1021
721	Qy	CGATGGAGGCATCTAGTCTGACCTGCTGCTGCTGCT	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	

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[illegible]

RESULT 8  
US-10-811-012-1  
; Sequence 1, Application US/10811012  
; Publication No. US20040152189A1  
; GENERAL INFORMATION:  
; APPLICANT: Geron Corporation  
; APPLICANT: McWhir, Jim  
; APPLICANT: Gold, Joseph D.  
; APPLICANT: Schiff, J. Michael  
; TITLE OF INVENTION: Selective Antibody Targeting of Undifferentiated Stem Cells  
; FILE REFERENCE: 096.006D- Sequelist  
; CURRENT APPLICATION NUMBER: US/10/811,012  
; CURRENT FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER: 09/995,419  
; PRIOR FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 60/253,357  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/253,443  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/253,395  
; PRIOR FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 15418  
; TYPE: DNA

; ORGANISM: Homo sapiens  
 US-10-811-012-1

	Query Match	100.0%;	Score 1001;	DB 7;	Length 15418;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1001;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AAAAGACCAGCATTTGGCACCCCTGGGACATTTGGCCCCACAGCCCTCGGAAATTCACCTGAC	60		
DB	9500	AAAAGACCAGCATTTGGCACCCCTGGGACATTTGGCCCCACAGCCCTCGGAAATTCACCTGAC	9559		
QY	61	TACGCACATCATGTATACACATCTCCGGTCCACGACCGACCCCGCTGTTTTATTTAATAGC	120		
DB	9560	TACGCACATCATGTATACACATCTCCGGTCCACGACCGACCCCGCTGTTTTATTTAATAGC	9619		
QY	121	TACAAAGCAGGAAATCCCTGCTAAATGTCCTTTAACCAACCTGGTTAAACAAACGGGTC	180		
DB	9620	TACAAAGCAGGAAATCCCTGCTAAATGTCCTTTAACCAACCTGGTTAAACAAACGGGTC	9679		
QY	181	CATCCGCA CGGTGGACAGTTCTCTCACAGTGAAGAGCAACATGCGGTTTTATAAGCCCTGCA	240		
DB	9680	CATCCGCA CGGTGGACAGTTCTCTCACAGTGAAGAGCAACATGCGGTTTTATAAGCCCTGCA	9739		
QY	241	GGCATCTCAAGGGAAATTAAGTGAAGTCAAAATCTGCCACCTCAATGGGATACGTAGCGCAAC	300		
DB	9740	GGCATCTCAAGGGAAATTAAGTGAAGTCAAAATCTGCCACCTCAATGGGATACGTAGCGCAAC	9799		
QY	301	ATGCTCAAAAGAAAGAAATTTACCCCATGGCAGGGGAGTGGTTGGGGGTTTAAGGACGG	360		
DB	9800	ATGCTCAAAAGAAAGAAATTTACCCCATGGCAGGGGAGTGGTTGGGGGTTTAAGGACGG	9859		
QY	361	TGGGGGCGAGCAGCTGGGGGCTATGTGACGACACCTTTACTAAAGCCAGTTTCTCGTTCT	420		
DB	9860	TGGGGGCGAGCAGCTGGGGGCTATGTGACGACACCTTTACTAAAGCCAGTTTCTCGTTCT	9919		
QY	421	GATGGTATTGGCTCAGTTATGGGAGCTAAACATAGGGGAGTGGGGAAACCCGG	480		
DB	9920	GATGGTATTGGCTCAGTTATGGGAGCTAAACATAGGGGAGTGGGGAAACCCGG	9979		
QY	481	AGGCTGTGCCATCTTTGCCATGCCCGAGTGCTCTGGCAGGATATGCTTAGAGATGCC	540		
DB	9980	AGGCTGTGCCATCTTTGCCATGCCCGAGTGCTCTGGCAGGATATGCTTAGAGATGCC	10039		
QY	541	CACGTCCTGATTTCCCCAAACCTGTGGAAGAAGCCCGCCCGCCCGGCTTTGCAGG	600		
DB	10040	CACGTCCTGATTTCCCCAAACCTGTGTGGAAGAAGCCCGCCCGGCTTTGCAGG	10099		
QY	601	TGTGATCTCGTGAGACCCCTGAGGTCTGGGATCTCTCGGGAATACCTGCAGGCCCGAAA	660		
DB	10100	TGTGATCTCGTGAGACCCCTGAGGTCTGGGATCTCTCGGGAATACCTGCAGGCCCGAAA	10159		
QY	661	AGTAATCCAGGGGTTCTGGGAAGAGCGGGCAGGAGGTCTAGAGGGGGGAGCCTCAGGA	720		
DB	10160	AGTAATCCAGGGGTTCTGGGAAGAGCGGGCAGGAGGTCTAGAGGGGGGAGCCTCAGGA	10219		
QY	721	CGATGAGGACAGTCAGTCTGAGGCTGAAAAGGAGGAGGAGGCTTCGAGCCCGAGGCTGCA	780		
DB	10220	CGATGAGGACAGTCAGTCTGAGGCTGAAAAGGAGGAGGAGGCTTCGAGCCCGAGGCTGCA	10279		
QY	781	AGGCCCTCAGAGCTGGAAAAGCGGGGAAGGGAACCTTCCA CGGAGCCTTCAGCAGGAA	840		
DB	10280	AGGCCCTCAGAGCTGGAAAAGCGGGGAAGGGAACCTTCCA CGGAGCCTTCAGCAGGAA	10339		
QY	841	GGCAGGGCTGGCCCTTTAGCCCAACAGGGCCCATCGTGGACCTCCGGGCTCCGTCGCATAG	900		
DB	10340	GGCAGGGCTGGCCCTTTAGCCCAACAGGGCCCATCGTGGACCTCCGGGCTCCGTCGCATAG	10399		
QY	901	GAGGGCACTCGCGCTGCCCTTCTAGCATGAAGTGTGGGATTTGCAAGCAACAGGA	960		
DB	10400	GAGGGCACTCGCGCTGCCCTTCTAGCATGAAGTGTGGGATTTGCAAGCAACAGGA	10459		
QY	961	AAACCATGCACTGTGAATCTAGGATTTATTTCAAACAAAGG	1001		

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US-09-995-419A-1  
 ; Sequence 1, Application US/09995419A  
 ; Publication No. US20030032187A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Geron Corporation  
 ; APPLICANT: McWhir, Jim  
 ; APPLICANT: Gold, Joseph D.  
 ; APPLICANT: Schiffe, J. Michael  
 ; TITLE OF INVENTION: 096,004 - SeqList  
 ; FILE REFERENCE: 096,004 - SeqList  
 ; CURRENT APPLICATION NUMBER: US/09/995,419A  
 ; CURRENT FILING DATE: 2001-11-26  
 ; PRIOR APPLICATION NUMBER: 60/253,357  
 ; PRIOR FILING DATE: 2000-11-27  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 15418  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-995-419A-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAGACCCAGCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 180  
 DB 9500 AAAAGACCCAGCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9599  
 Y 61 TAGCCATCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 120  
 DB 9560 TAGCCATCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9619  
 Y 121 TACAAAGCAGGAAATTCCTGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 180  
 DB 9620 TACAAAGCAGGAAATTCCTGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9679  
 Y 181 TAGCCATCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 240  
 DB 9680 TAGCCATCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9739  
 Y 241 GGCATCTCAAGGAAATTCCTGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 300  
 DB 9740 GGCATCTCAAGGAAATTCCTGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9799  
 Y 301 ATGCTCAAAAGAAAGAAATTCACCCATGCGAGGGGAGTGGTTGGGGGGTTAAGGACGG 360  
 DB 9500 AAAAGACCCAGCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9599  
 Y 61 TAGCCATCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 120  
 DB 9560 TAGCCATCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9619  
 Y 121 TACAAAGCAGGAAATTCCTGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 180  
 DB 9620 TACAAAGCAGGAAATTCCTGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9679  
 Y 181 TAGCCATCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 240  
 DB 9680 TAGCCATCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9739  
 Y 241 GGCATCTCAAGGAAATTCCTGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 300  
 DB 9740 GGCATCTCAAGGAAATTCCTGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9799  
 Y 301 ATGCTCAAAAGAAAGAAATTCACCCATGCGAGGGGAGTGGTTGGGGGGTTAAGGACGG 360

QY 721 CGATGAGGCGAGTCAGTCTGAGGCTGAAAAAGGAGGAGGAGGCTCGAGCCCGAGCTGCA 780  
 DB 10220 CGATGAGGCGAGTCAGTCTGAGGCTGAAAAAGGAGGAGGAGGCTCGAGCCCGAGCTGCA 10279  
 QY 781 AGCGCTCTCCAGAGCTGGAAGAGCGGGAAGGAGGAGGCTCCACGAGGCTGACAGGAA 840  
 DB 10280 AGCGCTCTCCAGAGCTGGAAGAGCGGGAAGGAGGAGGCTCCACGAGGCTGACAGGAA 10339  
 QY 841 GGCACGCGCTGCGCTTGTAGCCCTTACAGCCACAGGCGCCCATGCTGCGGCTCGTCCCATAG 900  
 DB 10340 GGCACGCGCTGCGCTTGTAGCCCTTACAGCCACAGGCGCCCATGCTGCGGCTCGTCCCATAG 10399  
 QY 901 GAGGCGCATGCGCTGCGCTTGTAGCATGAAGTGTGTGGGGATTTGAGAGCAACAGGA 960  
 DB 10400 GAGGCGCATGCGCTGCGCTTGTAGCATGAAGTGTGTGGGGATTTGAGAGCAACAGGA 10459  
 QY 961 AACCCATGCACTGTGAATCTAGGATTTATTTCAAAACAAAGG 1001  
 DB 10460 AACCCATGCACTGTGAATCTAGGATTTATTTCAAAACAAAGG 10500

## RESULT 4

US-10-141-220-1  
 ; Sequence 1, Application US/10141220  
 ; Publication No. US20030040111A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Geron Corporation  
 ; APPLICANT: Gold, Joseph  
 ; APPLICANT: Lebkowski, Jane  
 ; TITLE OF INVENTION: TPACKED stem cells  
 ; FILE REFERENCE: 096/003  
 ; CURRENT APPLICATION NUMBER: US/10/141,220  
 ; CURRENT FILING DATE: 2002-05-07  
 ; PRIOR APPLICATION NUMBER: US/09/783,203  
 ; PRIOR FILING DATE: 2001-02-13  
 ; PRIOR APPLICATION NUMBER: 60/253,443  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/253,357  
 ; PRIOR FILING DATE: 2000-11-27  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 15418  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-141-220-1

Query Match 100.0%; Score 1001; DB 5; Length 15418;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAGACCCAGCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 60  
 DB 9500 AAAAGACCCAGCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9599  
 QY 61 TAGCCATCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 120  
 DB 9560 TAGCCATCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9619  
 QY 121 TACAAAGCAGGAAATTCCTGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 180  
 DB 9620 TACAAAGCAGGAAATTCCTGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9679  
 QY 181 TAGCCATCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 240  
 DB 9680 TAGCCATCATGTCACACCTCCGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9739  
 QY 241 GGCATCTCAAGGAAATTCCTGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 300  
 DB 9740 GGCATCTCAAGGAAATTCCTGCTTAAATGCTTAAACAACTGGTTAAACAAACGGGTC 9799  
 QY 301 ATGCTCAAAAGAAAGAAATTCACCCATGCGAGGGGAGTGGTTGGGGGGTTAAGGACGG 360

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